

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:00 ; Search time 106.537 Seconds  
(without alignments)  
1187.771 Million cell updates/sec

Title: US-10-781-181-3  
Perfect score: 1540  
Sequence: 1 MSCLMVERCGEILLFENPDQN.....GTWDFDIFLDRLTNGNSLV 288

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	288	3 AAY93568	Aay93568 Amino aci
2	1430	92.9	268	3 AAY93593	Aay93593 Amino aci
3	1430	92.9	450	3 AAY93569	Aay93569 Amino aci
4	1430	92.9	450	4 AAU08675	Aau08675 Human pho
5	1430	92.9	450	4 AAG78915	Aag78915 Human typ
6	1430	92.9	450	8 ADP79549	Adp79549 Human pho
7	1376	89.4	446	3 AAY93567	Aay93567 Amino aci
8	1356	88.1	445	3 AAY93573	Aay93573 Amino aci
9	1356	88.1	446	3 AAY93574	Aay93574 Amino aci
10	1356	88.1	451	3 AAY93575	Aay93575 Amino aci
11	1337	86.8	437	3 AAY93572	Aay93572 Amino aci
12	1280	83.1	320	4 AAB36504	Aab36504 Human sho
13	1280	83.1	320	8 ADJ58906	Adj58906 Human cyc
14	1280	83.1	502	5 ABB09005	Abb09005 Human pho
15	1280	83.1	502	8 ADJ58904	Adj58904 Human cyc
16	1262	81.9	502	4 AAB36503	Aab36503 Human lon
17	1259.5	81.8	413	3 AAB36571	Aab36571 Amino aci
18	1145	74.4	391	4 AAU08676	Aau08676 Human pho
19	980	63.6	335	9 ADY50214	Ady50214 Human PDE
20	980	63.6	335	9 ADZ46770	Adz46770 Human PDE
21	913	59.3	456	5 AAE24530	Aae24530 Mouse PDE
22	907	58.9	424	5 AAU79727	Aau79727 Human cyc
23	907	58.9	432	4 AAU16967	Aau16967 Human nov
24	907	58.9	482	5 AAE24531	Aae24531 Human PDE

25	907	58.9	482	8 ADO40842	Ado40842 Human pho
26	907	58.9	482	8 ADR46207	Adr46207 Human pho
27	907	58.9	482	9 ADY18092	Ady18092 PRO polyp
28	907	58.9	498	2 AAU00094	Aau00094 CAMP phos
29	907	58.9	498	2 AAY49808	Aay49808 Human gli
30	907	58.9	498	3 AAB20619	Aab20619 pTM22 hum
31	907	58.9	498	3 ADR66097	Adr66097 Human pro
32	907	58.9	498	8 ADR66439	Adr66439 Human pro
33	906	58.8	456	8 ADO21910	Ado21910 Human CAM
34	906	58.8	456	9 ADY18172	Ady18172 PRO polyp
35	898	58.3	426	5 AAE24528	Aae24528 Mouse PDE
36	892	57.9	426	5 AAE24529	Aae24529 Rat PDE7
37	892	57.9	428	5 AAE24533	Aae24533 Rat PDE7a
38	891	57.9	426	5 AAE24527	Aae24527 Human PDE
39	891	57.9	426	5 AAE24532	Aae24532 Human PDE
40	890	57.8	441	8 ABM83121	Abm83121 Human dia
41	890	57.8	468	8 ABM83120	Abm83120 Human dia
42	807	52.4	424	5 AAU79713	Aau79713 Human pho
43	788	51.2	270	8 ADH61297	Adh61297 INTSIG pr
44	788	51.2	425	8 ABM83119	Abm83119 Human dia
45	772	50.1	437	8 ABM83118	Abm83118 Human dia

#### ALIGNMENTS

RESULT 1  
AAY93568  
ID AAY93568 standard; protein; 288 AA.  
XX  
AC AAY93568;  
XX  
DT 25-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of a human phosphodiesterase enzyme.  
XX  
KW Phosphodiesterase; PDE-XIV; human; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN EP1018559-A1.  
XX  
PD 12-JUL-2000.  
XX  
PF 09-NOV-1999; 99EP-00308902.  
XX  
PR 23-DEC-1998; 98GB-00028603.  
PR 17-SEP-1999; 99GB-00022123.  
XX  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
Fidock M;  
XX  
WFI; 2000-433274/38.  
DR N-PSDB; AAA46650.  
XX  
Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.  
XX  
Disclosure; Page 42-44; 104pp; English.  
XX  
The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and

CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
 CC gene and/or expression product may be used in the preparation of a  
 CC composition for the treatment of a disorder associated with inappropriate  
 CC PDE-XIV expression and/or activity and to screen for agents that can  
 CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
 CC may also be used as diagnostic agents for detecting the presence of PDE-  
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA))  
 XX  
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1540; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-162;  
 Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSCLWVERCGEILFENPDQNAKVCVCMGLDRLRGQTGVRAERGSYPFIDFRLNLTYS 60  
 Db 1 MSCLWVERCGEILFENPDQNAKVCVCMGLDRLRGQTGVRAERGSYPFIDFRLNLTYS 60  
 Qy 61 GEIGTKKKVKRLLSFORYPHARLLRGIIPQAPLHLLDELDYLGOARHMLSKVGMWDFDIF 120  
 Db 61 GEIGTKKKVKRLLSFORYPHARLLRGIIPQAPLHLLDELDYLGOARHMLSKVGMWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNS 240  
 Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNS 240  
 Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288  
 Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288

## RESULT 2

AA93593  
 ID AA93593 standard; protein; 268 AA.  
 XX  
 AC AA93593;  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human phosphodiesterase enzyme.  
 XX  
 KW Phosphodiesterase; PDE-XIV; enzyme.

XX Homo sapiens.  
 XX EP1018559-A1.  
 XX 12-JUL-2000.  
 XX 09-NOV-1999; 99EP-00308902.  
 XX 23-DEC-1998; 98GB-00028603.  
 XX 17-SEP-1999; 99GB-00022123.  
 XX (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.  
 XX Fidoack M;  
 XX WPI; 2000-433274/38.  
 XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
 XX useful for preventing diagnosing and treating diseases associated with  
 XX inappropriate PDE-XIV expression and/or activity.  
 XX Disclosure; Page 87-88; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE) enzyme. The  
 CC phosphodiesterase polynucleotide and polypeptide may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
 CC administered to treat diseases by rectifying mutations or deletions in a  
 CC patient's genome that affect the activity of PDE-XIV. They may also be  
 CC used to study the expression and function of PDE-XIV polypeptides and  
 CC their role in metabolism. The PDE-XIV polypeptides may be used as  
 CC antigens in the production of antibodies against PDE-XIV and in assays to  
 CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
 CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
 CC gene and/or expression product may be used in the preparation of a  
 CC composition for the treatment of a disorder associated with inappropriate  
 CC PDE-XIV expression and/or activity and to screen for agents that can  
 CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
 CC may also be used as diagnostic agents for detecting the presence of PDE-  
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA))  
 XX  
 SQ Sequence 268 AA;

Query Match 92.9%; Score 1430; DB 3; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-149;  
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSCLWVERCGEILFENPDQNAKVCVCMGLDRLRGQTGVRAERGSYPFIDFRLNLTYS 60  
 Db 1 MSCLWVERCGEILFENPDQNAKVCVCMGLDRLRGQTGVRAERGSYPFIDFRLNLTYS 60  
 Qy 61 GEIGTKKKVKRLLSFORYPHARLLRGIIPQAPLHLLDELDYLGOARHMLSKVGMWDFDIF 120  
 Db 61 GEIGTKKKVKRLLSFORYPHARLLRGIIPQAPLHLLDELDYLGOARHMLSKVGMWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNS 240  
 Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNS 240  
 Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268  
 Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

## RESULT 3

AA93569  
 ID AA93569 standard; protein; 450 AA.  
 XX  
 AC AA93569;  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human phosphodiesterase enzyme.  
 XX  
 KW Phosphodiesterase; PDE-XIV; human; enzyme.

XX Homo sapiens.  
 XX EP1018559-A1.  
 XX 12-JUL-2000.  
 XX 09-NOV-1999; 99EP-00308902.  
 XX 23-DEC-1998; 98GB-00028603.  
 XX 17-SEP-1999; 99GB-00022123.  
 XX (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.

PI Fidock M;  
XX WPI; 2000-433274/38.  
DR N-PSDB; AAA46651.  
XX  
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
PT useful for preventing diagnosing and treating diseases associated with  
PT inappropriate PDE-XIV expression and/or activity.  
XX  
XX PS Disclosure; Page 45-47; 104pp; English.  
XX  
XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
CC administered to treat diseases by rectifying mutations or deletions in a  
CC patient's genome that affect the activity of PDE-XIV. They may also be  
CC used to study the expression and function of PDE-XIV polypeptides and  
CC their role in metabolism. The PDE-XIV polypeptides may be used as  
CC antigens in the production of antibodies against PDE-XIV and in assays to  
CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
CC gene and/or expression product may be used in the preparation of a  
CC composition for the treatment of a disorder associated with inappropriate  
CC PDE-XIV expression and/or activity and to screen for agents that can  
CC modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies  
CC may also be used as diagnostic agents for detecting the presence of PDE-  
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
CC (ELISA))  
XX  
XX Sequence 450 AA;  
Query Match 92.9%; Score 1430; DB 3; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.8e-149;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTGVRAERGSYPFIDFRLNSTTYS 60  
DB 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTGVRAERGSYPFIDFRLNSTTYS 60  
QY 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIIPQAPHLHLLDEYLGQARHMLSKVGWDFDIF 120  
DB 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIIPQAPHLHLLDEYLGQARHMLSKVGWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
DB 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
QY 181 VTQAMHCYLKEPKLASFLTPDLIDMLGLLAAAHDVDHPGVNQPFLLIKTNHLLANLYQNM 240  
DB 181 VTQAMHCYLKEPKLASFLTPDLIDMLGLLAAAHDVDHPGVNQPFLLIKTNHLLANLYQNM 240  
QY 241 VLENHWRSTIGMLRESRLAHLPKEMT 268  
DB 241 VLENHWRSTIGMLRESRLAHLPKEMT 268  
RESULT 4  
AAU08675  
ID AAU08675 standard; protein; 450 AA.  
XX  
XX AAU08675;  
XX  
XX 18-DEC-2001 (first entry)  
XX Human phosphodiesterase type 7B #1.  
XX Human; phosphodiesterase type 7B; cardiovascular disease; asthma;  
KW allergy; inflammatory disease; immune-related disorder; cardiovascular;  
KW antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.  
XX  
XX Homo sapiens.

XX PN WO200162940-A2.  
XX PD 30-AUG-2001.  
XX  
XX 20-FEB-2001; 2001WO-EP001858.  
XX  
XX 21-FEB-2000; 2000EP-00103655.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
XX Kluxen F, Hentsch B;  
XX WPI; 2001-570636/64.  
XX N-PSDB; AAS13248.  
XX  
XX Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,  
PT diagnosing and treating, e.g. asthma, inflammation and allergies.  
XX  
XX Claim 1; Page 36-37; 40pp; English.  
XX  
XX The invention relates to a novel human Phosphodiesterase type 7B  
CC polypeptide and the nucleic acid that encodes it. The protein and nucleic  
CC acid may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For  
CC example, The protein and nucleic acid may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of P7B by expressing  
CC inactive proteins or to supplement the patients own production of P7B.  
CC The nucleic acids may be used to produce P7B polypeptides, by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. The nucleic acid and its complements may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar nucleic acids in samples, and therefore which patients may be in  
CC need of restorative therapy. The P7B polypeptides may also be used as  
CC antigens in the production of antibodies against P7B and in assays to  
CC identify modulators of its expression and activity. The anti-P7B  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-P7B antibodies may also be used as diagnostic  
CC agents for detecting the presence of P7B in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA)). Disorders that may be prevented,  
CC diagnosed and/or treated by the above methods include, for example  
CC cardiovascular disease, asthma, allergy, inflammation, and immune-related  
CC disorders. The present sequence represents a human phosphodiesterase 7B  
XX  
XX Sequence 450 AA;  
Query Match 92.9%; Score 1430; DB 4; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.8e-149;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTGVRAERGSYPFIDFRLNSTTYS 60  
DB 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTGVRAERGSYPFIDFRLNSTTYS 60  
QY 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIIPQAPHLHLLDEYLGQARHMLSKVGWDFDIF 120  
DB 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIIPQAPHLHLLDEYLGQARHMLSKVGWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
DB 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
QY 181 VTQAMHCYLKEPKLASFLTPDLIDMLGLLAAAHDVDHPGVNQPFLLIKTNHLLANLYQNM 240  
DB 181 VTQAMHCYLKEPKLASFLTPDLIDMLGLLAAAHDVDHPGVNQPFLLIKTNHLLANLYQNM 240  
QY 241 VLENHWRSTIGMLRESRLAHLPKEMT 268  
DB 241 VLENHWRSTIGMLRESRLAHLPKEMT 268  
RESULT 5

AAG78915  
ID AAG78915 standard; protein; 450 AA.  
XX AC  
XX AAG78915;  
XX AC  
XX 19-DEC-2001 (first entry)  
DT XX  
XX DE  
XX DE  
XX Human type 7B phosphodiesterase, PDE7B.  
XX KW  
XX Human; type 7B phosphodiesterase; PDE7B; enzyme.  
XX OS  
XX Homo sapiens.  
XX OS  
XX JP2001238680-A.  
XX PN  
XX 04-SEP-2001.  
XX PD  
XX 03-MAR-2000; 2000JP-00058159.  
XX PF  
XX 03-MAR-2000; 2000JP-00058159.  
XX PR  
XX (TANA ) TANABE SEIYAKU CO.  
XX PA  
XX WPI; 2001-610057/70.  
XX DR  
XX N-PSDB; AA170009.  
XX DR  
XX New phosphodiesterase for use in the development of inhibitors of high  
PT selectivity and drugs of low side effect.  
XX PT  
XX Claim 2; Page 12-14; 18pp; Japanese.  
XX PS  
XX The present sequence is the protein sequence for human type 7B  
CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the  
CC development of inhibitors of high selectivity and drugs of low side  
CC effects  
XX CC  
XX Sequence 450 AA;  
SQ  
Query Match 92.9%; Score 1430; DB 4; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.8e-149;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSCLMVERCGEILFENPDQNAKVCVCMGLDIRLGRGTGVAERRGSYPPFIDFRLINSTTYS 60  
DB 1 MSCLMVERCGEILFENPDQNAKVCVCMGLDIRLGRGTGVAERRGSYPPFIDFRLINSTTYS 60  
QY 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPOAPLHLLDELDYLGOARHMLSKVGWDFDIF 120  
DB 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPOAPLHLLDELDYLGOARHMLSKVGWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180  
DB 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180  
QY 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240  
DB 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240  
QY 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268  
DB 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268  
RESULT 6  
ADP79549  
ID ADP79549 standard; protein; 450 AA.  
XX AC  
XX ADP79549;  
XX AC  
XX 04-NOV-2004 (first entry)  
DT XX  
XX Human phosphodiesterase 7B nucleotide sequence.  
XX DE  
XX

KW Human; phosphodiesterase 7B; PDE7b; cardiovascular-gen.; CNS-Gen.;  
KW gynaecological; haemostatic; respiratory-Gen.; cytostatic; gene therapy;  
KW enzyme.  
XX Homo sapiens.  
XX OS  
XX WO2004044196-A1.  
XX PN  
XX 27-MAY-2004.  
XX PD  
XX 05-NOV-2003; 2003WO-EP012342.  
XX PF  
XX 13-NOV-2002; 2002EP-00025502.  
XX PR  
XX (FARB ) BAYER HEALTHCARE AG.  
XX PA  
XX Golz S, Brueggemeier U, Summer H;  
XX PI  
XX WPI; 2004-440631/41.  
XX DR  
XX N-PSDB; ADP79548.  
XX DR  
XX Screening for therapeutic agents, useful in treating cardiovascular,  
PT reproduction, urological, hematological, respiratory system or cancer  
PT diseases, comprises contacting a test compound with a phosphodiesterase  
PT 7b.  
XX PT  
XX Disclosure; SEQ ID NO 2; 128pp; English.  
XX PS  
XX The present sequence is that of human phosphodiesterase 7b (PDE7b), an  
CC enzyme regulating intracellular levels of cAMP and cGMP. The invention  
CC relates to novel disease associations of PDE7b polynucleotides and  
CC polypeptides. It also relates to novel methods of screening for  
CC therapeutic agents for the treatment of cardiovascular diseases,  
CC disorders of the peripheral and central nervous system, reproduction  
CC diseases, urological diseases, hematological diseases, disorders of the  
CC respiratory system and cancer. PDE7b polynucleotides, polypeptides and  
CC regulators or modulators of PDE7b activity (e.g. an RNA molecule,  
CC antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used  
CC in the treatment or diagnosis of these diseases and disorders.  
XX CC  
XX Sequence 450 AA;  
SQ  
Query Match 92.9%; Score 1430; DB 8; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.8e-149;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSCLMVERCGEILFENPDQNAKVCVCMGLDIRLGRGTGVAERRGSYPPFIDFRLINSTTYS 60  
DB 1 MSCLMVERCGEILFENPDQNAKVCVCMGLDIRLGRGTGVAERRGSYPPFIDFRLINSTTYS 60  
QY 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPOAPLHLLDELDYLGOARHMLSKVGWDFDIF 120  
DB 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPOAPLHLLDELDYLGOARHMLSKVGWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180  
DB 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180  
QY 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240  
DB 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240  
QY 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268  
DB 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268  
RESULT 7  
AAY93567  
ID AAY93567 standard; protein; 446 AA.  
XX AC  
XX AAY93567;  
XX XX



25-SEP-2000 (first entry)  
Amino acid sequence of a murine phosphodiesterase enzyme.  
Phosphodiesterase; PDE-XIV; murine; enzyme.  
Mus sp.  
EPI018559-A1.  
12-JUL-2000.  
09-NOV-1999; 99EP-00308902.  
23-DEC-1998; 98GB-00028603.  
17-SEP-1999; 99GB-00022123.  
(PFIZ ) PFIZER LTD.  
(PFIZ ) PFIZER INC.  
Fidock M;  
WPI; 2000-433274/38.  
N-PSDB; AAA46649.  
Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.  
Disclosure; Page 39-41; 104pp; English.  
The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA))

Query Match 89.48; Score 1376; DB 3; Length 446;  
Best Local Similarity 95.18; Pred. No. 2.7e-143;  
Matches 255; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MSLMVERCEILPENPDQNAKVCMLGDIRLQGTGVAERGSYPFIDRLINSTYS 60  
DB 1 MSLMVERCEILPENPDQNAKVCMLGDIRLQGTGVAERGSYPFIDRLINSTYS 60  
QY 61 GEIGTKKKVRLLSFQRYFHASRLRGIIIPQAPLHLLDELDYLQARHLSKVGWDPDIF 120  
DB 61 GEIGTKKKVRLLSFQRYFHASRLRGIIIPQAPLHLLDELDYLQARHLSKVGWDPDIF 120  
QY 121 LFRLLTNGNSLVTLCHLFTNTHGLIHFFKLDMTVTLHFLVMQVDYHSQNPYHNAVAAD 180  
DB 121 LFRLLTNGNSLVTLCHLFTNTHGLIHFFKLDMTVTLHFLVMQVDYHSQNPYHNAVAAD 180  
QY 181 VTQAMHCYLKEPKLAFSLTLPDLMGLAAAHVDHPGVNQPFLIKTNHLLANLYQNM 240  
DB 181 VTQAMHCYLKEPKLAFSLTLPDLMGLAAAHVDHPGVNQPFLIKTNHLLANLYQNM 240

QY 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
DB 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
RESULT 8  
AAY93573  
ID AAY93573 standard; protein; 445 AA.  
XX AAY93573;  
XX 25-SEP-2000 (first entry)  
XX Amino acid sequence of a phosphodiesterase enzyme.  
XX Phosphodiesterase; PDE-XIV; enzyme.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 12 /label= Val, Ile  
FT Misc-difference 16 /label= Ser, Asn  
FT Misc-difference 18 /label= Glu, Asp  
FT Misc-difference 20..21 /label= Ser, Val, Asn, Ala  
FT /note= "these residues are a peptide comprising at least two or more of the above residues"  
FT Misc-difference 30 /label= Val, Ile  
FT Misc-difference 39 /label= Pro, Arg  
FT Misc-difference 56 /label= Asn, Ser  
FT Misc-difference 59 /label= His, Tyr  
FT Misc-difference 114 /label= Thr, Met  
FT Misc-difference 141 /label= Ser, Thr  
FT Misc-difference 169..169 /label= Gly, His, Ser, Gln  
FT /note= "these residues are a peptide comprising at least two or more of the above residues"  
FT Misc-difference 307..308 /label= Asp, Ala, Asn, Val  
FT /note= "these residues are a peptide comprising at least two or more of the above residues"  
FT Misc-difference 350 /label= Glu, Asp  
FT Misc-difference 379 /label= Ser, Thr  
FT Misc-difference 391 /label= His, Arg  
FT Misc-difference 404 /label= Gly, Ser  
FT Misc-difference 418..419 /label= Pro, Arg, Ser, Asn  
FT /note= "these residues are a peptide comprising at least two or more of the above residues"  
FT Misc-difference 423 /label= Ser, Arg  
FT Misc-difference 423 /label= Ser, Arg  
FT Misc-difference 427..428 /label= Ser, Gly, Pro, Asp, His, Gln  
FT /note= "these residues are a peptide comprising at least two or more of the above residues"  
FT Misc-difference 430 /label= His, Leu  
FT Misc-difference 433..434 /label= Gln, Gly, Thr, Pro, Ala  
FT

FT /note= "these residues are a peptide comprising at least  
FT two or more of the above residues"  
FT Misc-difference 436..437  
FT /label= Ser, Glu, Thr, Leu  
FT /note= "these residues are a peptide comprising at least  
FT two or more of the above residues"  
FT Misc-difference 440  
FT /note= "optionally absent"  
FT Misc-difference 443..444  
FT /label= Asp, Ser, Ala, Thr  
FT /note= "these residues are a peptide comprising at least  
FT two or more of the above residues"

EPI018559-A1.

12-JUL-2000.

09-NOV-1999; 99EP-00308902.

23-DEC-1998; 98GB-00028603.

17-SEP-1999; 99GB-00022123.

(PFIZ ) PFIZER LTD.

(PFIZ ) PFIZER INC.

Fidock M;

WPI; 2000-433274/38.

Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
useful for preventing diagnosing and treating diseases associated with  
inappropriate PDE-XIV expression and/or activity.

Disclosure; Page 64-66; 104pp; English.

The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
enzyme sequence is derived from a formula of the invention. The  
phosphodiesterase polynucleotide and polypeptide may be used in the  
prevention, treatment and diagnosis of diseases associated with  
inappropriate PDE-XIV expression. For example, the polynucleotide be  
administered to treat diseases by rectifying mutations or deletions in a  
patient's genome that affect the activity of PDE-XIV. They may also be  
used to study the expression and function of PDE-XIV polypeptides and  
their role in metabolism. The PDE-XIV polypeptides may be used as  
antigens in the production of antibodies against PDE-XIV and in assays to  
identify modulators (agonists and antagonists) of PDE-XIV expression and  
activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
gene and/or expression product may be used in the preparation of a  
composition for the treatment of a disorder associated with inappropriate  
PDE-XIV expression and/or activity and to screen for agents that can  
modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies  
may also be used as diagnostic agents for detecting the presence of PDE-  
XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
(ELISA))

SQ Sequence 445 AA;

Query Match 88.1%; Score 1356; DB 3; Length 445;

Best Local Similarity 95.1%; Pred. No. 4.5e-141;

Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSCLMVERCGEIIIFENPDONAKVCMLGDIRLRGQTGVRAERGSYPFIDFLLNSTTYS 60  
DB 1 MSCLMVERCGEXLFEPXPQXXKVCMLGDXLRGQTGVRAERGSYPFIDFLLNSTTYS 60  
QY 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120  
DB 61 GEIGTKKKVKRLLSFORYFHASRLLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCLHFNTHGLIIHHFKLDMDVTLHRFLVMVQEDYHSQNPYHNAVAAD 180  
DB 121 LFDRLTNGNSLVTLCLHFNTHGLIIHHFKLDMDVTLHRFLVMVQEDYHSQNPYHNAVAAD 180

QY 181 VTQAMCYLKEPKLASFLTPDLIMGLAAAAHVDHPGVNQPFLLIKTNHHLANLYQMS 240  
DB 181 VTQAMCYLKEPKLASFLTPDLIMGLAAAAHVDHPGVNQPFLLIKTNHHLANLYQMS 240  
QY 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
DB 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
RESULT 9  
ID AAY93574  
AC AAY93574;  
XX 25-SEP-2000 (first entry)  
DT Amino acid sequence of a phosphodiesterase enzyme.  
DE Phosphodiesterase; PDE-XIV; enzyme.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 12 /label= Val, Ile  
FT Misc-difference 16 /label= Ser, Asn  
FT Misc-difference 18 /label= Glu, Asp  
FT Misc-difference 20 /label= Ser, Val, Asn, Ala  
FT Misc-difference 21 /label= Ser, Val, Asn, Ala  
FT Misc-difference 30 /label= Val, Ile  
FT Misc-difference 39 /label= Pro, Arg  
FT Misc-difference 56 /label= Asn, Ser  
FT Misc-difference 59 /label= His, Tyr  
FT Misc-difference 114 /label= Thr, Met  
FT Misc-difference 141 /label= Ser, Thr  
FT Misc-difference 168 /label= Gly, His, Ser, Gln  
FT Misc-difference 169 /label= Gly, His, Ser, Gln  
FT Misc-difference 307 /label= Asp, Ala, Asn, Val  
FT Misc-difference 308 /label= Asp, Ala, Asn, Val  
FT Misc-difference 350 /label= Asp, Ala, Asn, Val  
FT Misc-difference 379 /label= Glu, Asp  
FT Misc-difference 391 /label= Ser, Thr  
FT Misc-difference 391 /label= His, Arg  
FT Misc-difference 404 /label= Gly, Ser  
FT Misc-difference 418 /label= Pro, Arg, Ser, Asn  
FT Misc-difference 419 /label= Pro, Arg, Ser, Asn  
FT Misc-difference 423 /label= Ser, Arg  
FT Misc-difference 430 /label= His, Leu  
FT Misc-difference 433 /label= Gln, Gly, Thr, Pro, Ala





PD 12-JUL-2000.  
XX  
PF 09-NOV-1999; 99EP-00308902.  
XX  
PR 23-DEC-1998; 98GB-00028603.  
PR 17-SEP-1999; 99GB-00022123.  
XX  
PA (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX  
FI Fidoack M;  
XX  
XX WPI; 2000-433274/38.  
XX  
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
PT useful for preventing diagnosing and treating diseases associated with  
PT inappropriate PDE-XIV expression and/or activity.  
XX  
XX  
PS Disclosure; Page 58-60; 104pp; English.  
XX  
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC enzyme sequence is derived from a formula of the invention. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
CC administered to treat diseases by rectifying mutations or deletions in a  
CC patient's genome that affect the activity of PDE-XIV. They may also be  
CC used to study the expression and function of PDE-XIV polypeptides and  
CC their role in metabolism. The PDE-XIV polypeptides may be used as  
CC antigens in the production of antibodies against PDE-XIV and in assays to  
CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
CC gene and/or expression product may be used in the preparation of a  
CC composition for the treatment of a disorder associated with inappropriate  
CC PDE-XIV expression and/or activity and to screen for agents that can  
CC modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies  
CC may also be used as diagnostic agents for detecting the presence of PDE-  
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
CC (ELISA)).  
XX  
SQ Sequence 437 AA;  
Query Match 86.8%; Score 1337; DB 3; Length 437;  
Best Local Similarity 95.1%; Pred. No. 5.7e-139;  
Matches 255; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
QY 1 MSCLMVERCGEILFENPDONAKVCMLGDIRLRCGTGVAERGSYPFIDFLLNSTYS 60  
DB 1 MSCLMVERCGEXLPFXQ-KKVCMLGDXRLRCGTGVAERGSYPFIDFLLNXTXS 59  
QY 61 GEIGTKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARMLSKVGWDFDIF 120  
DB 60 GEIGTKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARMLSKVGWDFDIF 119  
QY 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRFLVMVQEDYHSQNPYNHVAAD 180  
DB 120 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRFLVMVQEDYHX-NPYHNAVHAD 178  
QY 181 VTQAMHCYLPKPLASFLTPDIDIMGLLAAAHVDHPGVNQPFLIKTNHHLANLYQMS 240  
DB 179 VTQAMHCYLPKPLASFLTPDIDIMGLLAAAHVDHPGVNQPFLIKTNHHLANLYQMS 238  
QY 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
DB 239 VLENHWRSTIGMLRESRLLAHLPKEMT 266  
RESULT 12  
AAB36504  
ID AAB36504 standard; protein; 320 AA.  
XX  
AC AAB36504;

XX  
DT 06-MAR-2001 (first entry)  
XX  
DE Human short phosphodiesterase protein SEQ ID NO:3.  
XX  
KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;  
KW cyclic nucleotide phosphodiesterase; nootropic; cardiac; hypotensive;  
KW nephrotropic; antidepressant; antiinflammatory; immunosuppressive;  
KW antiinfertility; antiasthmatic; vasotropic; gene therapy; dementia;  
KW annesia; congestive heart failure; thrombosis; pulmonary hypertension;  
KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;  
KW atopic disease; autoimmune encephalomyelitis; organ transplantation;  
KW nephrotic syndrome; erectile dysfunction.  
XX  
OS Homo sapiens.  
XX  
PN US6146876-A.  
XX  
PD 14-NOV-2000.  
XX  
PF 11-JUN-1999; 99US-00330970.  
XX  
PR 26-MAR-1999; 99US-00277423.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Kapeller-Libermann R, White D, Robison KE;  
XX  
XX WPI; 2001-023577/03.  
DR N-PSDB; AAC87949.  
XX  
XX Polynucleotide encoding novel cyclic nucleotide phosphodiesterase useful  
PT for treating disorders related with to protein e.g. dementia,  
PT hypertension, glomerulonephritis, and organ transplantation.  
XX  
XX Claim 3; Fig 6; 42pp; English.  
XX  
CC The present sequence represents the human short phosphodiesterase which  
CC is a cyclic nucleotide phosphodiesterase (I). (I) can have nootropic,  
CC cardiac, hypotensive, nephrotropic, antidepressant, antiinflammatory,  
CC immunosuppressive, antiinfertility, antiasthmatic and vasotropic  
CC activities, and can be used in gene therapy. (I) can be used for treating  
CC various disorders associated or mediated by (I), such as dementia.  
CC annesia, congestive heart failure, thrombosis, pulmonary hypertension,  
CC glomerulonephritis, bipolar depression, bronchial asthma, atopic  
CC diseases, autoimmune encephalomyelitis, organ transplantation, salt  
CC retention in nephrotic syndrome and erectile dysfunction  
XX  
SQ Sequence 320 AA;  
Query Match 83.1%; Score 1280; DB 4; Length 320;  
Best Local Similarity 100.0%; Pred. No. 7.7e-133;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GDIRLRCGTGVAERGSYPFIDFLLNSTYSGEIGTKKVKRLLSFQRYFHASRLRG 87  
DB 80 GDIRLRCGTGVAERGSYPFIDFLLNSTYSGEIGTKKVKRLLSFQRYFHASRLRG 139  
QY 88 IIPQAPLHLLDEYLGQARMLSKVGWDFDIFLDRLTNGNSLVTLCHLNFTHGLIHH 147  
DB 140 IIPQAPLHLLDEYLGQARMLSKVGWDFDIFLDRLTNGNSLVTLCHLNFTHGLIHH 199  
QY 148 FKLDWVTLHRFLVMVQEDYHSQNPYNHVAADVTQAMHCYLPKPLASFLTPDIDIMGL 207  
DB 200 FKLDWVTLHRFLVMVQEDYHSQNPYNHVAADVTQAMHCYLPKPLASFLTPDIDIMGL 259  
QY 208 LAAAHVDHPGVNQPFLIKTNHHLANLYQMSVLENHWRSTIGMLRESRLLAHLPKEM 267  
DB 260 LAAAHVDHPGVNQPFLIKTNHHLANLYQMSVLENHWRSTIGMLRESRLLAHLPKEM 319  
QY 268 T 268  
DB 320 T 320

```
RESULT 13
ADJ58906
ID ADJ58906 standard; protein; 320 AA.
XX
AC ADJ58906;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human cyclic nucleotide phosphodiesterase protein #2.
XX
KW 27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;
KW cellular proliferation; cellular differentiation; immune disorder;
KW cardiovascular disorder; endothelial cell disorder;
KW haematopoietic disorder; blood vessel disorder; brain disorder; pain;
KW metabolic disorder; liver disorder; platelet disorder; gene therapy;
KW human; cyclic; enzyme.
XX
OS Homo sapiens.
XX
PN US2004006016-A1.
XX
PD 08-JAN-2004.
XX
PF 11-MAR-2003; 2003US-00386414.
XX
PR 11-JUN-1999; 99US-00330970.
XX
PR 25-OCT-1999; 99US-00426282.
XX
PR 16-MAY-2000; 2000US-00571689.
XX
PR 22-SEP-2000; 2000US-00668266.
XX
PR 28-NOV-2000; 2000US-00724599.
XX
PR 07-DEC-2000; 2000US-0254037P.
XX
PR 10-APR-2001; 2001US-00833082.
XX
PR 16-MAY-2001; 2001US-00860193.
XX
PR 31-OCT-2001; 2001US-0335044P.
XX
PR 06-DEC-2001; 2001US-00010943.
XX
PR 29-OCT-2002; 2002US-00283023.
XX
PA (WILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, White D, Robison KE, Macbeth KJ, Carroll JM;
PI Cook WJ, Meyers RE, Chun M, Williamson MJ;
XX
WPI: 2004-081738/08.
XX
N-PSDB; ADJ58905.
XX
PT New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic
PT acid molecules, useful for diagnosing or treating cancer, pain, or
PT immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
PT and liver disorders.
XX
Claim 4; SEQ ID NO 6; 245pp; English.
XX
The present invention relates to an isolated 27875, 22025, 27420, 17906,
CC 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for
CC diagnosing or treating cancer or aberrant cellular proliferation and/or
CC differentiation, immune disorders, heart disorders, cardiovascular
CC disorders including endothelial cell disorders, haematopoietic disorders,
CC blood vessel disorders, brain disorders, pain and metabolic disorders,
CC liver disorders and platelet disorders. The invention is also useful in
CC gene therapy. The present sequence is human cyclic nucleotide
CC phosphodiesterase.
XX
SQ Sequence 320 AA;
Query Match 83.1%; Score 1280; DB 8; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.7e-133;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 GDIRLRGQTGVARRGSGYPFIDRLNLTSTYSGETGKKVKRLLSFQRYFHASRLRG 87
DB 80 GDIRLRGQTGVARRGSGYPFIDRLNLTSTYSGETGKKVKRLLSFQRYFHASRLRG 139
```

```
QY 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFLRNLNGNSLVTLCHLFNTHGLIHH 147
DB 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFLRNLNGNSLVTLCHLFNTHGLIHH 199
QY 148 FKLDVMTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKPKLASFLTPDLMGL 207
DB 200 FKLDVMTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKPKLASFLTPDLMGL 259
QY 208 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 267
DB 260 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 319
QY 268 T 268
DB 320 T 320

RESULT 14
AB09005
ID AB09005 standard; protein; 502 AA.
XX
AC AB09005;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human phosphodiesterase-1.
XX
KW HPDE; human phosphodiesterase; cyclic nucleotide phosphodiesterase;
KW antiinflammatory; neuroprotective; cytostatic; antianaemic;
KW immunosuppressive; HIV; cardiovascular disorder; mental disorder;
KW gene therapy; transgene; enzyme.
XX
OS Homo sapiens.
XX
PN WO200198471-A2.
XX
PD 27-DEC-2001.
XX
PF 21-JUN-2001; 2001WO-US020140.
XX
PR 22-JUN-2000; 2000US-0213741P.
PR 14-JUL-2000; 2000US-0218234P.
PR 16-OCT-2000; 2000US-0241100P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Thornton M, Ding L, Patterson C, Yao MG, Tribouley CM, Lal P;
PI Hafalia AJA, Baughn MR, Ramkumar J, Lu Y, Walia NK;
XX
WPI: 2002-147799/19.
XX
N-PSDB; ABA99136.
XX
Novel human phosphodiesterase polypeptides and polynucleotides for
PT diagnosing, preventing and treating eye, neurological, cardiovascular,
PT cell proliferative and autoimmune/inflammatory disorders.
XX
Claim 1; Page 97-98; 105pp; English.
XX
This invention relates to isolated human phosphodiesterase polypeptides
CC (HPDE 1-4), which are antiinflammatory, neuroprotective, cytostatic,
CC antianaemic, immunosuppressive and anti-HIV in their action. The
CC polypeptides are useful for screening a compound for effectiveness as an
CC agonist or antagonist of the protein. The identified agonist, antagonist
CC and protein are useful for treating a disease or condition associated
CC with decreased or overexpression of functional HPDE in a patient. The
CC proteins are useful in preparing polyclonal or monoclonal antibodies by
CC hybridoma technology. They are also useful in the treatment and
CC prevention of eye, neurological, cardiovascular, cell proliferative and
CC autoimmune and inflammatory disorders, metabolic disorders and mental
CC disorders. The polynucleotides are useful for creating humanised animals
CC or transgenic animals to model human disease and to detect and quantify
CC gene expression in biopsied tissues in which expression of HPDE is
```

CC correlated with disease. HPDE, its fragments and antibodies specific for  
CC HPDE are useful as elements on a microarray which is useful to monitor or  
CC measure protein-protein interactions, drug-target interactions and gene  
CC expression profiles. This sequence represents HPDE-1

XX SQ Sequence 502 AA;

Query Match 83.1%; Score 1280; DB 5; Length 502;  
Best Local Similarity 100.0%; Pred. No. 1.5e-132;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDILRGQTGVRAERGSYPFIDFRLNLSNYSYGEIGTKKKVKKLLSFQRYFHASRLRG 87  
Db 80 GDILRGQTGVRAERGSYPFIDFRLNLSNYSYGEIGTKKKVKKLLSFQRYFHASRLRG 139  
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 199  
Qy 148 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDIMGL 207  
Db 200 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDIMGL 259  
Qy 208 LAAAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319  
Qy 268 T 268  
Db 320 T 320

RESULT 15

ADJ58904  
ID ADJ58904 standard; protein; 502 AA.

XX AC ADJ58904;

XX DT 06-MAY-2004 (first entry)

XX DE Human cyclic nucleotide phosphodiesterase protein #1.

XX KW 27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;  
KW cellular proliferation; cellular differentiation; immune disorder;  
KW cardiovascular disorder; endothelial cell disorder;  
KW haematopoietic disorder; blood vessel disorder; brain disorder; pain;  
KW metabolic disorder; liver disorder; platelet disorder; gene therapy;  
KW human; cyclic; enzyme.

XX OS Homo sapiens.

XX PN US2004006016-A1.

XX PD 08-JAN-2004.

XX PF 11-MAR-2003; 2003US-00386414.

XX PR 11-JUN-1999; 99US-00330970.

XX PR 25-OCT-1999; 99US-00426282.

XX PR 16-MAY-2000; 2000US-00571689.

XX PR 22-SEP-2000; 2000US-00668266.

XX PR 08-NOV-2000; 2000US-00724599.

XX PR 07-DEC-2000; 2000US-0254037P.

XX PR 10-APR-2001; 2001US-00833082.

XX PR 16-MAY-2001; 2001US-00860193.

XX PR 31-OCT-2001; 2001US-0335044P.

XX PR 06-DEC-2001; 2001US-00010943.

XX PR 29-OCT-2002; 2002US-00283023.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Kapeller-Libermann R, White D, Robison KE, Macbeth KJ, Carroll JM;

PI Cook WJ, Meyers RE, Chun M, Williamson MJ;

XX DR

WPI; 2004-081738/08.

DR N-PSDB; ADJ58903.

XX PT

New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecules, useful for diagnosing or treating cancer, pain, or immune, endothelial cell, haematopoietic, blood vessel, brain, metabolic and liver disorders.

XX PS

Claim 4; SEQ ID NO 4; 245pp; English.

XX CC

The present invention relates to an isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for diagnosing or treating cancer or aberrant cellular proliferation and/or differentiation, immune disorders, heart disorders, cardiovascular disorders including endothelial cell disorders, haematopoietic disorders, blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders and platelet disorders. The invention is also useful in gene therapy. The present sequence is human cyclic nucleotide phosphodiesterase.

XX SQ

Sequence 502 AA;

Query Match

83.1%; Score 1280; DB 8; Length 502;

Best Local Similarity 100.0%; Pred. No. 1.5e-132; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28

GDILRGQTGVRAERGSYPFIDFRLNLSNYSYGEIGTKKKVKKLLSFQRYFHASRLRG 87

Db 80

GDILRGQTGVRAERGSYPFIDFRLNLSNYSYGEIGTKKKVKKLLSFQRYFHASRLRG 139

Qy 88

IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 147

Db 140

IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148

FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDIMGL 207

Db 200

FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDIMGL 259

Qy 208

LAAAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267

Db 260

LAAAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy 268

T 268

Db 320

T 320

Search completed: March 10, 2006, 19:56:51

Job time : 109.537 secs



**this Page Blank (uspio)**

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:57:15 ; Search time 19.9024 Seconds  
(without alignments)  
1392.313 Million cell updates/sec

Title: US-10-781-181-3  
Perfect score: 1540  
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLRLTNGNSLV 288

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1430	92.9	450	2 JC7266	3',5'-cyclic-AMP nucle
2	907	58.9	498	2 A47286	3',5'-cyclic-AMP p
3	331.5	21.5	584	2 B53109	3',5'-cyclic-nucle
4	331.5	21.5	672	2 161259	3',5'-cyclic-nucle
5	330.5	21.5	673	2 161358	3',5'-cyclic-nucle
6	320.5	20.8	886	2 A54442	3',5'-cyclic-nucle
7	317.5	20.6	562	2 159143	CAMP phosphodiesterase
8	317.5	20.6	564	2 A40949	cyclic-AMP phospho
9	316.5	20.6	610	2 167946	3',5'-cyclic-nucle
10	316.5	20.6	844	2 153865	phosphodiesterase
11	314.5	20.4	564	2 JC1519	3',5'-cyclic-nucle
12	314.5	20.4	736	2 161354	phosphodiesterase
13	305	19.8	712	2 S71626	3',5'-cyclic-nucle
14	301.5	19.6	323	2 S55348	3',5'-cyclic-nucle
15	296.5	19.3	534	1 A44162	3',5'-cyclic-nucle
16	296.5	19.3	535	1 A46378	3',5'-cyclic-nucle
17	295.5	19.2	535	1 A44161	3',5'-cyclic-nucle
18	295	19.2	536	2 167945	3',5'-cyclic-nucle
19	291	18.9	519	2 T14783	hypothetical prote
20	285	18.5	713	2 JW0088	3',5'-cyclic-nucle
21	282.5	18.3	536	1 JC6129	3',5'-cyclic-nucle
22	281	18.2	549	2 T16769	hypothetical prote
23	279	18.1	664	2 T24459	hypothetical prote
24	278	18.1	530	1 A45334	3',5'-cyclic-nucle
25	269.5	17.5	659	2 JC0293	3',5'-cyclic-nucle
26	269.5	17.5	885	2 JC7858	3',5'-cyclic-nucle
27	268	17.4	777	2 S65543	3',5'-cyclic-nucle
28	263	17.1	768	2 T10796	3',5'-cyclic-nucle
29	258	16.8	491	2 A40283	3',5'-cyclic-nucle

30 246 16.0 267 2 B33904  
31 228.5 14.8 1054 2 T30901  
32 223.5 14.5 875 1 A48719  
33 223.5 14.5 875 1 JW0106  
34 216.5 14.1 259 2 T20399  
35 204 13.2 1108 2 A48508  
36 198.5 12.9 1112 2 S70522  
37 186 12.1 928 1 JC2486  
38 185 12.0 921 1 A40981  
39 180.5 11.7 853 2 A36617  
40 176.5 11.5 854 2 A42828  
41 176.5 11.5 856 1 A47451  
42 176 11.4 858 2 JC4520  
43 176 11.4 1141 2 A44093  
44 175.5 11.4 800 2 S13032  
45 175.5 11.4 856 2 S30762

ALIGNMENTS

RESULT 1  
JC7266  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human  
N;Alternate names: CAMP-specific phosphodiesterase 7B  
C;Species: Homo sapiens (man)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: JC7266  
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.  
Biochem. Biophys. Res. Commun. 271, 575-583, 2000  
A;Title: Identification of human PDE7B, a CAMP-specific phosphodiesterase.  
A;Reference number: JC7266  
A;Accession: JC7266  
A;Molecule type: mRNA  
A;Residues: 1-450 <SAS>  
A;Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040  
A;Experimental source: caudate nucleus  
C;Genetics:  
A;Gene: pde7B  
A;Map position: 6q23-24  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-cyclic-AMP phosphodiesterase (man)  
C;Keywords: phosphoric diester hydrolase

Query Match 92.9%; Score 1430; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 8.2e-121;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGTGVAERGSYFFIDRLNLTYS 60  
Db 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGTGVAERGSYFFIDRLNLTYS 60  
Qy 61 GEIGTKKVKRLSFGYFHASRLRLGRIPOAPLHLLDELYLQARHMLSKVGWDFDIF 120  
Db 61 GEIGTKKVKRLSFGYFHASRLRLGRIPOAPLHLLDELYLQARHMLSKVGWDFDIF 120  
Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMQEDYHSQNPYHNAHAAD 180  
Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMQEDYHSQNPYHNAHAAD 180  
Qy 181 VTQAMCYLKEPKLASFLPLDMLGLLAAAHDVDPGVNQPFLIKTNHLLANLYQNS 240  
Db 181 VTQAMCYLKEPKLASFLPLDMLGLLAAAHDVDPGVNQPFLIKTNHLLANLYQNS 240  
Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
Db 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 2  
A47286  
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 03-Nov-2000



```
Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPOAPLHLLDDEYLGQARHMLSKVGMWDFDIEL 121
Db 218 KKKKRPMSQISGVKKLMSLSSNSIPRGVKTQEDVLAKS---LEDVKNKGLHVR 274
Qy 122 FDLRTNGNSLVTLLCH-LFNTHGLIHHFKLDVTLHRLFLVMVQEDYHSONPYHNAVHAAD 180
Db 275 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDTLITYLTMTLEDHYHADVAHNNIHAAD 333
Qy 181 VTQAMHCYKPKLASFLTPDLMGLLAAAHVDVHPGVNQPLIKTNHHLANLYQNMS 240
Db 334 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHVDVHPGVSNQPLINTNSALMALMYNDSS 393
Qy 241 VLENHHRSTIGMLRE 256
Db 394 VLENHHLAVGPKLQ 409

RESULT 5
161358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human
N/Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C/Accession: I61358; I38416
R/Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A/Title: A family of human phosphodiesterases homologous to the dunce learning and memoi
A/Reference number: A54442; MUID:94019330; PMID:8413254
A/Accession: I61358
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-673 <RES>
R/Baecker, P.A.; Oberholte, R.; Bach, C.; Yes, C.; Shelton, E.R.
Gene 138, 253-256, 1994
A/Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodie
A/Reference number: I38416; MUID:94171048; PMID:8125310
A/Accession: I38416
A/Molecule type: mRNA
A/Residues: 70-507, 'P', 509-673 <RE2>
A/Cross-references: UNIPARC:UPI000016A067; EMBL:U02882; NID:9433346; PIDN:AA03592.1; PI
C/Genetics:
A/Gene: GDB:PDE4D; DPDE3
A/Cross-references: GDB:I32541; OMIM:600129
A/Map position: 5q12-5q12
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C/Keywords: cAMP binding; phosphoric diester hydrolase
F:325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 21.5%; Score 330.5; DB 2; Length 673;
Best Local Similarity 37.8%; Pred. No. 1.2e-21;
Matches 74; Conservative, 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPOAPLHLLDDEYLGQARHMLSKVGMWDFDIEL 121
Db 218 KKKKRPMSQISGVKKLMSLSSNSIPRGVKTQEDVLAKS---LEDVKNKGLHVR 274
Qy 122 FDLRTNGNSLVTLLCH-LFNTHGLIHHFKLDVTLHRLFLVMVQEDYHSONPYHNAVHAAD 180
Db 275 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDTLITYLTMTLEDHYHADVAHNNIHAAD 333
Qy 181 VTQAMHCYKPKLASFLTPDLMGLLAAAHVDVHPGVNQPLIKTNHHLANLYQNMS 240
Db 334 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHVDVHPGVSNQPLINTNSALMALMYNDSS 393
Qy 241 VLENHHRSTIGMLRE 256
Db 394 VLENHHLAVGPKLQ 409

RESULT 6
A54442
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice B
```

```
N/Contains: 3',5'-cyclic AMP phosphodiesterase HPDB4A6 splice form
C/Species: Homo sapiens (man)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: A54442; S55788; A36317; S55787
R/Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A/Title: A family of human phosphodiesterases homologous to the dunce learning and memoi
A/Reference number: A54442; MUID:94019330; PMID:8413254
A/Accession: A54442
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-886 <RES>
A/Cross-references: UNIPROT:P27815; UNIPARC:UPI0000047003; GB:L20965; NID:9347119; PIDN:
R/Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.
Cell. Signal. 6, 793-812, 1994
A/Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a h
A/Reference number: S55788; MUID:95194817; PMID:7888306
A/Accession: S55788
A/Molecule type: mRNA
A/Residues: 'MCPFPVTV', 210-735, 'E', 737-886 <SUL>
A/Cross-references: UNIPARC:UPI000002A6CE; EMBL:U18087; NID:9604374; PIDN:AA050458.1; PI
A/Note: 736-Ala was also found
R/Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Davi
Mol. Cell. Biol. 10, 2678-2686, 1990
A/Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic A
A/Reference number: A36317; MUID:90258854; PMID:2160582
A/Accession: A36317
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 'MCPFPVTV', 210-516, 'Y', 518-722, 'R', 724-736, 'R', 728-735, 'E', 737-788, 'E', 790-
A/Cross-references: UNIPARC:UPI000017C062; GB:M37744
C/Genetics:
A/Gene: GDB:PDE4A; DPDE2
A/Cross-references: GDB:138776; OMIM:600126
A/Map position: 19p13.1-19q12
C/Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F:432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.8%; Score 320.5; DB 2; Length 886;
Best Local Similarity 35.1%; Pred. No. 1.3e-20;
Matches 66; Conservative 38; Mismatches 81; Indels 3; Gaps 1;

Qy 69 VKRLSFQRYFHASRLRLGIIPOAPLHLLDDEYLGQARHMLSKVGMWDFDIFDLRTNG 128
Db 332 MSQITGLKMLHNSLNSNIPRGVKTQEDVLELAQELNLK---WGLNIFCVSDYAGG 388
Qy 129 NSLVTLTCLHFNTHGLIHHFKLDVTLHRLFLVMVQEDYHSONPYHNAVHAADVTQAMHCY 188
Db 389 RSLTCINMYLFQERDLTKFKRIPVDVTWYTLTDHYHADVAHNSLHAADVLSQSTVL 448
Qy 189 LKEPKLASFLTPDLMGLLAAAHVDVHPGVNQPLIKTNHHLANLYQNMSVLENHHR 248
Db 449 LATPALDAVFTDLEILAAIFASAIHVDVHPGVSNQPLINTNSALMALMYNDESVLENHHLA 508
Qy 249 STIGMLRE 256
Db 509 VGPKLQ 516

RESULT 7
I59143
cAMP phosphodiesterase - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59143
R/Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A/Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAM
A/Reference number: I59143; MUID:89264471; PMID:2542941
A/Accession: I59143
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-562 <RES>
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Db 118 AQELENLSK---WGLNIFCVSEYAGRSLSICIMYTIQFERDLLKKFHPVDVTMMYMLTL 174  
Qy 163 QEDYHSQNPYHVAADVTQAMHCYKLPKASFLTPDLIMGLLAAAHADVDHGPVQ 222  
Db 175 EDHYHADVAYHNSLHAADVLQSTHVLATPALDAVFTDLSEILAAFAAAIHVDHGPVSN 234  
Qy 223 PFLIKTHHLANLYONMSVLENHHRSTIGMLRE 256  
Db 235 QFLINTSELALMYNDSVLENHHLAVGFKLQE 268

RESULT 10  
153865  
phosphodiesterase - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: J53865  
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.  
Gene 149, 237-244, 1994  
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gene  
A;Reference number: I53865; MUID:95047482; PMID:7958996  
A;Accession: J53865  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-844 <RES>  
A;Cross-references: UNIPROT:P54748; UNIPARC:UPI0000127BF5; GB:L27057; NID:G3334904; PIDN:  
F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.6%; Score 316.5; DB 2; Length 844;  
Best Local Similarity 33.2%; Pred. No. 2.9e-20;  
Matches 71; Conservative 32; Mismatches 86; Indels 25; Gaps 2;

Qy 43 RGSYPFDPLRLNSTYSGIGTKKVKRLLSFORYPHASRLRLGIIPOAPLHLLDSDYL 102  
Db 314 RQSQPMESQITGLKKLVHTGSLNTN-----VPRFGVKTQDQDL 351

Qy 103 GOARHMSKVGMDPDIPLDRLTNGNSLVTLCHLNFTHGLIHHFKLDMVTLHRLVMV 162  
Db 352 AQELENLSK---WGLNIFCVSEYAGRSLSICIMYTIQFERDLLKKFHPVDVTMMYMLTL 408

Qy 163 QEDYHSQNPYHVAADVTQAMHCYKLPKASFLTPDLIMGLLAAAHADVDHGPVQ 222  
Db 409 EDHYHADVAYHNSLHAADVLQSTHVLATPALDAVFTDLSEILAAFAAAIHVDHGPVSN 468

Qy 223 PFLIKTHHLANLYONMSVLENHHRSTIGMLRE 256  
Db 469 QFLINTSELALMYNDSVLENHHLAVGFKLQE 502

RESULT 11  
JC1519  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBP106) -  
C;Species: Homo sapiens (man)  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C;Accession: JC1519; A45500; I61359  
R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, K.  
Gene 129, 239-247, 1993  
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a  
A;Reference number: JC1519; MUID:93314968; PMID:8392015  
A;Accession: JC1519  
A;Molecule type: mRNA  
A;Residues: 1-564 <OBE>  
A;Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014C5AB; GB:L12686  
A;Experimental source: lymphocyte  
A;Note: only partial nucleotide sequence is given  
R;McLaughlin, M.M.; Ciebski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.;  
J. Biol. Chem. 268, 6470-6476, 1993  
A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.  
f mRNA  
A;Reference number: A45500; MUID:93203241; PMID:8394210  
A;Accession: A45500  
A;Molecule type: mRNA  
A;Residues: 1-564 <MCL>

A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:G292387; PIDN:AAA36426.1; PID:  
A;Experimental source: frontal cortex  
A;Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBIP:127930)  
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory  
A;Reference number: A54442; MUID:94019330; PMID:8413254  
A;Accession: I61359  
A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-564 <RES>  
A;Cross-references: UNIPARC:UPI000014C5AB; GB:L20971; NID:G347131; PIDN:AAA03593.1; PID:  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C;Keywords: phosphoric diester hydrolase  
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.4%; Score 314.5; DB 2; Length 564;  
Best Local Similarity 33.6%; Pred. No. 2.6e-20;  
Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPOAPLHLLDDEYLGQARHMSKVGWDFDIFL 121  
Db 126 KKKKQQLMTQISGVKKLMHSSLNNTSISRFVNTENEDHLAKELEDLNK---WGLNIFN 182

Qy 122 FDLRTNGNSLVTLCHLNFTHGLIHHFKLDMVTLHRLVMVQSDYHSQNPYHVAADV 181  
Db 183 VAGYSHNRPLTCIMYAFQERDLTKFRISSTDFITYMTLEDHYSDVAYHNSLHAADV 242

Qy 182 TQAMHCYKLPKASFLTPDLIMGLLAAAHADVDHGPVQNPFLIKTHHLANLYONMSV 241  
Db 243 AQSTHVLSTPALDAVFTDLSEILAAFAAAIHVDHGPVSNQFLINTSELALMYNDSV 302

Qy 242 LENHHRSTIGMLRESR--LLAHLPKEMTGT 270  
Db 303 LENHHLAVGFKLQERHCDIFMNLTKKQRT 333

RESULT 12  
I61354  
phosphodiesterase - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I61354  
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory  
A;Reference number: A54442; MUID:94019330; PMID:8413254  
A;Accession: I61354  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-736 <RES>  
A;Cross-references: UNIPROT:Q07343; UNIPARC:UPI0000127BF6; GB:L20966; NID:G347121; PIDN:  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.4%; Score 314.5; DB 2; Length 736;  
Best Local Similarity 33.6%; Pred. No. 3.6e-20;  
Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPOAPLHLLDDEYLGQARHMSKVGWDFDIFL 121  
Db 298 KKKKQQLMTQISGVKKLMHSSLNNTSISRFVNTENEDHLAKELEDLNK---WGLNIFN 354

Qy 122 FDLRTNGNSLVTLCHLNFTHGLIHHFKLDMVTLHRLVMVQSDYHSQNPYHVAADV 181  
Db 355 VAGYSHNRPLTCIMYAFQERDLTKFRISSTDFITYMTLEDHYSDVAYHNSLHAADV 414

Qy 182 TQAMHCYKLPKASFLTPDLIMGLLAAAHADVDHGPVQNPFLIKTHHLANLYONMSV 241  
Db 415 AQSTHVLSTPALDAVFTDLSEILAAFAAAIHVDHGPVSNQFLINTSELALMYNDSV 474

Qy 242 LENHHRSTIGMLRESR--LLAHLPKEMTGT 270  
Db 303 LENHHLAVGFKLQERHCDIFMNLTKKQRT 333

Db 475 LENHHLAVGFKLLQBEHCIDIFMNLTKKQRT 505

RESULT 13

S71626

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human

N;Alternate names: 3',5'-cyclic AMP phosphodiesterase

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004

C;Accession: S71626; 161356

R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.

FEBS Lett. 358, 305-310, 1995

A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific p

A;Reference number: S71626; MUID:95145731; PMID:7843419

A;Accession: S71626

A;Molecule type: DNA

A;Residues: 1-712 <ENG>

A;Cross-references: UNIPROT:Q08493; UNIPARC:UPI0000163B31; EMBL:Z46632; NID:G727222; PID

A;Experimental source: substantia nigra

R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,

Mol. Cell. Biol. 13, 6558-6571, 1993

A;Title: A family of human phosphodiesterases homologous to the dunce learning and memoi

A;Reference number: A54442; MUID:94019330; PMID:8413254

A;Accession: I61356

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 462-712 <RES>

A;Cross-references: UNIPARC:UPI000016AE86; GB:I20968; NID:G347125; PIDN:AAA03591.1; PID:

C;Genetics:

A;Gene: HSPDE4C1

C;Function:

A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP

A;Pathway: cyclic nucleotide metabolism

A;Note: expressed in various tissues but not in cells of the immune system

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C;Keywords: phosphoric diester hydrolase

F;387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 19.8%; Score 305; DB 2; Length 712;

Best Local Similarity 28.5%; Pred. No. 2.5e-19;

Matches 76; Conservative 44; Mismatches 107; Indels 40; Gaps 5;

QY 11 EILFENPDQNAKVCMLGDIRLGQGVRAERGSYPFIDFRLN-----STTYSG-- 61

Db 204 KLAETLDELDCDQLETLQTRHSVGMASNFK-----RLNRELTHLSETSRGQ 257

QY 62 -----ETGTYK-----KVRLLSFQRYFHASRLLRGIPOAPLHLDE 99

Db 258 VSEYISRTFLDQTEVELPKVTAEEAPQPMRSIRSLGLHGLSASLSSATVPREGVQTDQE 317

QY 100 DYLGQARHMLSKYGMWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHHFKLDNVTLHREL 159

Db 318 EQAKE---LEDNKNWGLDVKVADVSGNRP/LTAIIFSIFQERDLTKTFOIPADTLATYL 374

QY 160 VMQEDYHSONPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIMLGLLAAAHHVDVHPG 219

Db 375 LMLEGHYHANVAHNSLHAADVAQSTHVLATPALEAVFTDLEILAAALFASAIHVDVHPG 434

QY 220 VNQPFLLKTNHHLANLYQNMSVLENH 246

Db 435 VSNQFLINTNSDVALMYNDASVLENH 461

RESULT 14

S55348

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) HSPDE4A7 - human

N;Alternate names: 3',5'-cyclic AMP phosphodiesterase

C;Species: Homo sapiens (man)

C;Date: 23-Aug-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S55348

R;Horton, Y.M.; Sullivan, M.; Houslay, M.D.

Biochem. J. 308, 683-691, 1995

A;Title: Molecular cloning of a novel splice variant of human type IV(A) (PDE-IV(A)) cyd

A;Reference number: S55348; MUID:95290008; PMID:7772058

A;Accession: S55348

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-323 <HOR>

A;Cross-references: UNIPROT:P27815; UNIPARC:UPI000002A6D0; EMBL:U18088; NID:G604376; PID:

C;Keywords: phosphoric diester hydrolase

F;98-312/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 19.8%; Score 301.5; DB 2; Length 323;

Best Local Similarity 37.3%; Pred. No. 1.8e-19;

Matches 66; Conservative 32; Mismatches 72; Indels 7; Gaps 4;

QY 83 RLIRGGII--POAPLHLLDEYLGQARHM--LSKVGWMDFDIFLFDRLTNGNSLVTLCHLF 139

Db 10 KLGNVLQGP--PYRLTSS---GLRLHQELENKNGLNIFCVSDYAGGSLTCIMTMIF 65

QY 140 NTHGLIHHFKLDNVTLHRLVMVQEDYHSONPYHNAVHAADVTQAMHCYLKEPKLASFLT 199

Db 66 QERDLKKFRIPVDTWVTYMLTLEDHYHADVAHNSLHAADVLQSTHVLATPALDAVFT 125

QY 200 PLDIMLGLLAAAHHVDVHPGVNPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRE 256

Db 126 DLEILAAFAAAIHDVDHFGVSNQFLINTNSALMYNDESIVLENHHLAVGFKLLQE 182

RESULT 15

A44162

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp

N;Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C;Accession: A44162; B40283

R;Bentley, J.K.; Kadlecek, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,

J. Biol. Chem. 267, 18676-18682, 1992

A;Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodiester

A;Reference number: A44162; MUID:92406781; PMID:1326531

A;Accession: A44162

A;Molecule type: mRNA

A;Residues: 1-534 <BEN>

A;Cross-references: UNIPROT:Q01061; UNIPARC:UPI0000127BEB; GB:M94867; NID:G162782; PIDN:

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIPI:113352)

R;Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.

Biochemistry 30, 7940-7947, 1991

A;Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc

A;Reference number: A40283; MUID:91329366; PMID:1651112

A;Accession: B40283

A;Molecule type: protein

A;Residues: 29-45,'IP', 48,'R', 50-52,'IS', 55-85;196-215;277,'D', 279,'T', 281-287,'T', 289-2;

A;Cross-references: UNIPARC:UPI0000144B58; UNIPARC:UPI000017288B; UNIPARC:UPI000017288C;

A;Experimental source: brain

C;Comment: This enzyme is a useful target for inducing the death of leukemic cells, and t

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C;Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h

F;220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 19.3%; Score 296.5; DB 1; Length 534;

Best Local Similarity 37.9%; Pred. No. 1e-18;

Matches 61; Conservative 30; Mismatches 67; Indels 3; Gaps 2;

QY 109 LSKVGWMDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHHFKLDNVTLHRLVMVQEDYHS 168

Db 156 LKNVDLFCDFVSLNRAADDHALRTIVFELLTRHNLISRFKPTVFLMTFLDLALETGYCK 215

QY 169 -QNYPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIMLGLLAAAHHVDVHPGVNQPFLIK 227

Db 216 YKNYPYHNAVHAADVTQVHCFLRLRTGMVHCLSEIVLAIIFAAAIDHYEHTGTTSFHIQ 275

QY 228 TNHHLANLYQNMSVLENHHRSTIGMLR--ESRLLAHLPE 266

Db 276 TKSECAILYNDRSVLENHHSVFRMMQDDEMNIFINLTKD 316



Search completed: March 10, 2006, 20:03:02  
Job time : 22.9024 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:25 ; Search time 120.195 Seconds  
(without alignments)  
1690.519 Million cell updates/sec

Title: US-10-781-181-3

Perfect score: 1540

Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1430	92.9	450	1 PDE7B_HUMAN	Q9np56 homo sapien
2	1430	92.9	450	2 Q5VWY9_HUMAN	Q5VWY9 homo sapien
3	1376	89.4	446	1 PDE7B_MOUSE	Q9gxi1 mus musculus
4	1376	89.4	446	2 Q8CB82_MOUSE	Q8CB82 mus musculus
5	1367	88.8	446	2 Q8VIE4_RAT	Q8VIE4 rattus norv
6	1350.5	87.7	459	2 Q8VIE2_RAT	Q8VIE2 rattus norv
7	1280	83.1	586	2 Q4LE81_HUMAN	Q4LE81 homo sapien
8	999.5	64.9	456	2 Q4RR95_TETNG	Q4RR95 tetraodon n
9	953	61.9	359	2 Q8VIE3_RAT	Q8VIE3 rattus norv
10	914	59.4	482	2 Q6P5G2_MOUSE	Q6P5G2 mus musculus
11	913	59.3	456	1 PDE7A_MOUSE	P70453 mus musculus
12	907	58.9	424	2 Q96T72_HUMAN	Q96T72 homo sapien
13	907	58.9	482	1 PDE7A_HUMAN	Q13946 homo sapien
14	906	58.8	456	2 Q5R5B5_PONPY	Q5R5B5 pongo pygma
15	892	57.9	426	1 PDE7A_RAT	Q08593 rattus norv
16	775	50.3	381	2 Q505M0_XENLA	Q505M0 xenopus lae
17	711	46.2	199	2 Q4VX30_HUMAN	Q4VX30 homo sapien
18	595	38.6	324	2 Q4R6T4_XACPA	Q4R6T4 macaca fasc
19	475	30.8	305	2 Q7PNE5_ANOGA	Q7PNE5 anopheles g
20	409	26.6	162	2 Q86V65_HUMAN	Q86V65 homo sapien
21	331.5	21.5	747	1 PDE4D_MOUSE	Q10163 mus musculus
22	331.5	21.5	803	1 PDE4D_RAT	P14270 rattus norv
23	330.5	21.5	809	1 PDE4D_HUMAN	Q08499 homo sapien
24	325.5	21.1	682	2 Q5XGT5_XENLA	Q5XGT5 xenopus lae
25	320.5	20.8	563	2 Q5ZKR6_CHICK	Q5ZKR6 gallus gall
26	320.5	20.8	647	2 Q8IV47_HUMAN	Q8IV47 homo sapien
27	320.5	20.8	825	2 Q9H3H2_HUMAN	Q9H3H2 homo sapien
28	320.5	20.8	860	2 Q5DM53_HUMAN	Q5DM53 homo sapien
29	320.5	20.8	864	2 Q6PMT2_HUMAN	Q6PMT2 homo sapien
30	320.5	20.8	886	1 PDE4A_HUMAN	P27815 homo sapien
31	319.5	20.7	1051	2 Q4SML2_TETNG	Q4SML2 tetraodon n

32	318.5	20.7	721	2 Q9OXI7_MOUSE	Q9OXI7 mus musculus
33	317.5	20.6	383	2 Q8QB2_MOUSE	Q8QB2 mus musculus
34	317.5	20.6	503	2 Q6IQY6_MOUSE	Q6IQY6 mus musculus
35	317.5	20.6	542	2 Q91VY2_MOUSE	Q91VY2 mus musculus
36	317.5	20.6	659	2 Q8VD81_RAT	Q8VD81 rattus norv
37	317.5	20.6	721	1 PDE4B_RAT	P14646 rattus norv
38	317.5	20.6	721	2 Q8VBU5_MOUSE	Q8VBU5 mus musculus
39	317.5	20.6	722	2 Q5RKL0_RAT	Q5RKL0 rattus norv
40	317.5	20.6	736	2 Q8VD82_RAT	Q8VD82 rattus norv
41	317.5	20.6	867	2 Q4RL51_TETNG	Q4RL51 tetraodon n
42	316.5	20.6	771	2 Q9EQR7_RAT	Q9EQR7 rattus norv
43	316.5	20.6	844	1 PDE4A_RAT	P54748 rattus norv
44	314.5	20.4	518	2 Q43850_HUMAN	Q43850 homo sapien
45	314.5	20.4	564	2 Q5T3Z8_HUMAN	Q5T3Z8 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	PDE7B_HUMAN	STANDARD;	PRT;	450 AA.
AC	Q9NP56,			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).			
GN	Name=PDE7B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
EX	MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;			
RA	Sasaki T., Kotera J., Yuasa K., Omori K.;			
RT	"Identification of human PDE7B, a CAMP-specific phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 271:575-583(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Fetal brain;			
EX	MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;			
RA	Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;			
RT	"Cloning and characterisation of the human and mouse PDE7B, a novel			
RL	CAMP-specific nucleotide phosphodiesterase.";			
RC	Biochem. Biophys. Res. Commun. 272:186-192(2000).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Brain;			
EX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RT	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RL	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Small D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences.";			
RC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

-!- FUNCTION: May be involved in the control of CAMP-mediated neural



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20087273; PubMed=10618442; DOI=10.1073/pnas.97.1.472;  
 RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;  
 RT "Cloning and characterization of PDE7B, a cAMP-specific  
 phosphodiesterase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J;  
 RA Gardner C.E., Robas N.M., Cawkill D., Fiddock M.D.;  
 RT "Cloning and characterization of the human and mouse PDE7B, a novel  
 cAMP-specific nucleotide phosphodiesterase.";  
 RL Biochem. Biophys. Res. Commun. 272:186-192(2000).  
 CC -1- FUNCTION: May be involved in the control of cAMP-mediated neural  
 activity and cAMP metabolism in the brain.  
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =  
 adenosine 5'-phosphate.  
 CC -1- COFACTOR: Divalent cations (By similarity).  
 CC -1- ENZYME REGULATION: Inhibited by dipyradimole, IBMX and SCH51866.  
 CC -1- SENSITIVE TO zaprinast, rolipram, and milrinone.  
 CC -1- PATHWAY: Cyclic nucleotide metabolism.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in brain.  
 CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two  
 putative divalent metal sites and an N-terminal regulatory domain.  
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR ENBL; AF190639; AAF25195.1; -; mRNA.  
 DR ENBL; AJ251859; CAB92530.1; -; mRNA.  
 DR HSP; Q08499; IOYN.  
 DR Ensemble; ENSMUSG00000019990; Mus musculus.  
 DR GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.  
 DR MGI; MGI:1352752; Pde7b.  
 DR InterPro; IPR02073; PDEase.  
 DR Pfam; PF00233; PDEase\_I; 1.  
 DR PRINTS; PRO0387; PDIESTERASE1.  
 DR PROSITE; PS00126; PDEASE\_I; 1.  
 KW cAMP; Hydrolyase.  
 FT REGION 172 410 Catalytic (By similarity).  
 SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;  
 Query Match 89.4%; Score 1376; DB 1; Length 446;  
 Best Local Similarity 95.1%; Pred. No. 5e-117;  
 Matches 255; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 MSCLMVRCCEILLFENPDQNAKVCVCMGLDIRLGRGTGVAERGSYPFIDFRLNNTYS 60  
 Db 1 MSCLMVRCCEILLFENPDQNAKVCVCMGLDIRLGRGTGVAERGSYPFIDFRLNNTYS 60  
 Qy 61 GEIGTKKKVRLLSFQRYFHASRLLRGTIIQAPLHLLDELDYLGOARHLSKVGWDFDIF 120  
 Db 61 GEIGTKKKVRLLSFQRYFHASRLLRGTIIQAPLHLLDELDYLGOARHLSKVGWDFDIF 120  
 Qy 121 LFDRLTNGSLVTLCHLNFTHGLIHHFKLDMVTLHRLFLVWQSDYHSQPNVNAHAAD 180  
 Db 121 LFDRLTNGSLVTLCHLNFTHGLIHHFKLDMVTLHRLFLVWQSDYHSQPNVNAHAAD 180  
 Qy 181 VTQAMHCYLPKPKLAFSLTFLDLMGLLAAAHVDHPGVNQPPLIKTNHLLANLYQMS 240  
 Db 181 VTQAMHCYLPKPKLAFSLTFLDLMGLLAAAHVDHPGVNQPPLIKTNHLLANLYQMS 240

Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMT 268  
 RESULT 4  
 Q8CBS2\_MOUSE  
 ID Q8CBS2\_MOUSE PRELIMINARY; PRT; 446 AA.  
 AC Q8CBS2;  
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Mus musculus adult male urinary bladder cDNA, RIKEN full-length  
 DE enriched library, clone:9530027016 product:phosphodiesterase 7B, full  
 DE insert sequence.  
 GN Name=Pde7b;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl L.M., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schraml L.M., Staubli R., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;

```

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tegami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK035385; BAC29052.1; -; mRNA.
DR HSSP; Q08499; IOYN.
DR MGI; MGI:1352752; Pde7b.
DR GO; GO:0004115; F:camp-specific phosphodiesterase activity; IDA.
DR InterPro; IPR003607; Met_phos_hydro.
DR Pfam; PF002073; PDEase.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 446 AA; 51307 MW; 7C002364B396A5A8 CRC64;

Query Match 89.4%; Score 1376; DB 2; Length 446;
Best Local Similarity 95.1%; Pred. No. 5e-117; Indels 0; Gaps 0;
Matches 255; Conservative 8; Mismatches 5;

Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLLNSTYS 60
Db 1 MSCLMVERCGEVLFPESQSVKVCMLGDLVRLRGQTGVPAERGSYPFIDFRLLNNTS 60

Qy 61 GEIGTKKKVKRLLSFORYFHASLLRGIIPQAPLHLLDEYLGQARHMLSKVGWDFDIF 120
Db 61 GEIGTKKKVKRLLSFORYFHASLLRGIIPQAPLHLLDEYLGQARHMLSKVGWDFDIF 120

Qy 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180
Db 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

Qy 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180
Db 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 5
Q8VIE4_RAT PRELIMINARY; PRT; 446 AA.
ID Q8VIE4_RAT PRELIMINARY; PRT; 459 AA.
AC Q8VIE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17).
GN Names=Pde7b; Synonyms=RNPDE7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057411; BAB79639.1; -; mRNA.
DR HSSP; Q08499; IOYN.
DR Ensemble; ENSRNOG00000013436; Rattus norvegicus.
DR RGD; 621016; Pde7b.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057409; BAB79637.1; -; mRNA.
DR HSSP; Q08499; IOYN.
DR Ensemble; ENSRNOG00000013436; Rattus norvegicus.
DR RGD; 621016; Pde7b.
DR GO; GO:0004114; F:3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phos_hydro.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 446 AA; 51475 MW; 01567BDABC905D19 CRC64;

Query Match 88.8%; Score 1367; DB 2; Length 446;
Best Local Similarity 94.0%; Pred. No. 3.3e-116; Indels 0; Gaps 0;
Matches 252; Conservative 10; Mismatches 6;

Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLLNSTYS 60
Db 1 MSCLMVERCGEVLFPENPEQNVKVCMLGDLVRLRGQTGVPAERGSYPFIDFRLLNNTS 60

Qy 61 GEIGTKKKVKRLLSFORYFHASLLRGIIPQAPLHLLDEYLGQARHMLSKVGWDFDIF 120
Db 61 GEIGTKKKVKRLLSFORYFHASLLRGIIPQAPLHLLDEYLGQARHMLSKVGWDFDIF 120

Qy 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180
Db 121 LPDLRTNGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLIMLGLLAAAHDVDPHGVNQPFLLKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 6
Q8VIE2_RAT PRELIMINARY; PRT; 459 AA.
ID Q8VIE2_RAT PRELIMINARY; PRT; 459 AA.
AC Q8VIE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).
GN Names=Pde7b; Synonyms=RNPDE7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057411; BAB79639.1; -; mRNA.
DR HSSP; Q08499; IOYN.
DR Ensemble; ENSRNOG00000013436; Rattus norvegicus.
DR RGD; 621016; Pde7b.

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DR GO: 0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a...; IEA.  
DR GO: 0016787; F-hydrolase activity; IEA.  
DR GO: 0007165; P-signal transduction; IEA.  
DR InterPro: IPR003607; Met\_phos\_hydro.  
DR Pfam: PF00233; PDEase.  
DR PRINTS: PR00387; PDIESTERASEL.  
DR SMART: SMO0471; HDC; 1.  
DR PROSITE: PS00126; PDEASE\_I; UNKNOWN\_1.  
DR KEGG: Hydrolase.  
SQ SEQUENCE 459 AA; 52680 MW; A3F26E95C7FC00A5 CRC64;  
  
Query Match 87.7%; Score 1350.5; DB 2; Length 459;  
Best Local Similarity 89.7%; Pred. No. 1.1e-114;  
Matches 252; Conservative 10; Mismatches 6; Indels 13; Gaps 1;  
  
QY 1 MSCLMVERGEIIFENPDONAKVCVML-----GDRLRGOTGVRAERGSGYP 47  
DB 1 MSCLMVERGEVLFENPEQNKVCVCMALASSPPPLPMAGQGVDVRURGTGVPAERGSYP 60  
  
QY 48 FIDFRLLNSTTYSGETIGTKKKVKRLLSFORYFHASRLLRGIIPQAPHLHLLDEDYLQARH 107  
DB 61 FIDFRLLNTHTSGETISGSKKKVKRLLSFORHPHESRLLRGMTQPAPHLHLLDEDYLQARH 120  
  
QY 108 MLSKVGMWDFDIFDLRLTNGLNSLVTLCHLNFTHGLIHFFKLDVMVTLHRFLVMVQEDYH 167  
DB 121 MLSKVGMWDFDIFDLRLTNGLNSLVTLCHLNFTHGLIHFFKLDVMVTLHRFLVMVQEDYH 180  
  
QY 168 SQNPYNNAHAADVTQAMHCYLKEPKLASFLPDLIMLGSLAAAHVDHDPGVNQPFILIK 227  
DB 181 GHNPYNNAHAADVTQAMHCYLKEPKLASFLPDLIMLGSLAAAHVDHDPGVNQPFILIK 240  
  
QY 228 TNHHLANLYQNMSVLNHNHWSTIGMRESRLLAHLPKEMT 268  
DB 241 TNHHLANLYQNMSVLNHNHWSTIGMRESRLLAHLPKEMT 281  
  
RESULT 7  
Q4LE81 HUMAN  
ID Q4LE81\_HUMAN PRELIMINARY; PRT; 586 AA.  
AC Q4LE81  
DT 13-SEP-2005 (TEMBLrel. 31, Created)  
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)  
DE PDE7B variant protein (Fragment).  
GN Names=PDE7B variant protein;  
OS Homo sapiens (Human);  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN NCBI  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,  
RA Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;  
RT "Preparation of a set of expression-ready clones of mammalian long  
RT cDNAs encoding large proteins by the ORF trap cloning method."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.  
DR ENBL; AB209990; BAE06072.1; -, mRNA.  
FT NON TER 1  
SQ SEQUENCE 586 AA; 66230 MW; F96F4F0549AFE8D CRC64;  
  
Query Match 83.1%; Score 1280; DB 2; Length 586;  
Best Local Similarity 100.0%; Pred. No. 4.2e-108;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 28 GDRLRGOTGVRAERGSYPFDIFRLNLTSSGIBTGKVKRLLSFORYFHASRLLRG 87  
DB 164 GDRLRGOTGVRAERGSYPFDIFRLNLTSSGIBTGKVKRLLSFORYFHASRLLRG 223  
  
QY 88 IIPQAPHLHLLDEDYLQARHMLSKVGMDPDFLFDRLTNGLNSLVTLCHLNFTHGLIH 147

Df Db Qy 224 IIPQAPHLHLLDEDYLQARHMLSKVGMDPDFLFDRLTNGLNSLVTLCHLNFTHGLIH 207  
Qy 148 FKLDVMVTLHRFLVMVQEDYHSQNPYNNAHAADVTQAMHCYLKEPKLASFLPDLIMLGSL 343  
Db 284 FKLDVMVTLHRFLVMVQEDYHSQNPYNNAHAADVTQAMHCYLKEPKLASFLPDLIMLGSL 267  
Qy 208 LAAAAHDVDHPGVNQPFILKTNNHLLANLYQNMSVLNHNHWSTIGMRESRLLAHLPKEM 403  
Db 344 LAAAAHDVDHPGVNQPFILKTNNHLLANLYQNMSVLNHNHWSTIGMRESRLLAHLPKEM 268  
Qy 268 T 268  
Db 404 T 404  
  
RESULT 8  
Q4RR95 TETNG  
ID Q4RR95\_TETNG PRELIMINARY; PRT; 456 AA.  
AC Q4RR95  
DT 13-SEP-2005 (TEMBLrel. 31, Created)  
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)  
DE Chromosome 14 SCAP15003, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNAMES=GSTENG0030267001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OC NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lucifalla G., Dossat N., Castellano B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kallias M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype."  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Genoscope; Whitehead  
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC ENBL; CAAG01015003; CAG09087.1; -, Genomic\_DNA.  
FT NON TER 1  
FT NON TER 456 456  
SQ SEQUENCE 456 AA; 52118 MW; 60B4805381D70669 CRC64;  
  
Query Match 64.9%; Score 999.5; DB 2; Length 456;  
Best Local Similarity 67.0%; Pred. No. 1.3e-82;  
Matches 195; Conservative 32; Mismatches 35; Indels 29; Gaps 6;  
  
QY 7 ERCGEITLPNDONAKVCVML-----GDITL-RGQTGV-RAERGSYP 47  
DB 1 ORCGAVLTSPQNAVQRMLDRHVRNRPHLPAASTAECCKLSKGAGVILLVERGSYP 60  
  
QY 48 FIDFRLLNSTTYSGETI--GTTKKVKRLLSFORYFHASRLLRGIIPQAP--LHLLDEDYL 103  
DB 61 LDLOQLVKSQQSGEVASTGRKRVORQSFBRYCHASRLLRGLVPAPLSHLDDGYLG 120  
  
QY 104 QARHMLSKVGMDPDFLFDRLTNGLNSLVTLCHLNFTHGLIHFFKLDVMVTLHRFLVMVQ 163



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Db 121 QAAHMLSKVGTWTFDIFLFDRLTNGSLVTLNCHLFNVYGLVHFQFQDLMVKLHFLGKVVQ 180
Qy 164 EDYHSQNPYHNAHAADVQAMHCYLYKEPKCLASFLTPDLMGLLAAAHADVDPHPGVNQP 223
Db 181 EDYHSQNPYHNAHAADVQAMHCYLYKEPKCLAEQLSPDVLFLJMAAAAHADVDPHPGVNQP 240
Qy 224 FLIKTNHLLANLY-----QNMVLENHHRSTTCMLRRESRLLAHLPKEMT 268
Db 241 FLIKTRHLLASLYQHVSQVNTSVLESHHWRSTVGMLRESGLSLHLPADM 291

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## RESULT 9

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ID Q8VIE3 RAT PRELIMINARY; PRT; 359 AA.
AC Q8VIE3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B3 (EC 3.1.4.17).
GN Name=Pde7b; Synonym=RNPD7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057410; BAB79638.1; -; mRNA.
DR HSSP; Q08499; 10YN.
DR RGD; 621016; Pde7b.
DR GO; GO:0004114; F3; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 359 AA; 41456 MW; 0FF72792737CE48A CRC64;

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Query Match 61.9%; Score 953; DB 2; Length 359;
Best Local Similarity 98.3%; Pred. No. 1.8e-78;
Matches 176; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 90 POAPLHLLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHHFK 149
Db 3 POAPLHLLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHHFK 62

Qy 150 LDMVTLHRLFLVMVQEDYHSQNPYHNAHAADVQAMHCYLYKEPKCLASFLTPDLMGLLA 209
Db 63 LDMVTLHRLFLVMVQEDYHGNPYHNAHAADVQAMHCYLYKEPKCLASFLTPDLMGLLA 122

Qy 210 AAADVDPHPGVNQPFLIKTNHLLANLYQNMSVLENHHRSTTCMLRRESRLLAHLPKEMT 268
Db 123 AAADVDPHPGVNQPFLIKTNHLLANLYQNMSVLENHHRSTTCMLRRESRLLAHLPKEMT 181

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## RESULT 10

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Q6P5G2 MOUSE PRELIMINARY; PRT; 482 AA.
ID Q6P5G2_MOUSE PRELIMINARY;
AC Q6P5G2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pde7a protein.
GN Name=Pde7a;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC MDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugin T.B., Toohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062809; AAH62809.1; -; mRNA.
DR MGI; MGI:1202402; Pde7a.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 482 AA; 55189 MW; F8460D84BFE7B65 CRC64;

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Query Match 59.4%; Score 914; DB 2; Length 482;
Best Local Similarity 65.8%; Pred. No. 9.4e-75;
Matches 171; Conservative 36; Mismatches 53; Indels 0; Gaps 0;

Qy 7 ERCEILFENPDQNAKVCVCMGLDIRLQGTVRAERGSYPFDIFRLNSTTYSGEIGTK 66
Db 46 QRRGALSVDSSDQATLYIRMLGDVVRVRAGPETERRGSHPIIDFRIFHSQSDIEASVSA 105

Qy 67 KKKVRLLSQRFPHASRLRGRIPOAPLHLLDDEYLGQARHMLSKVGMWDFDIFLFDRLT 126
Db 106 RNIRRLLSQRFYLRSSRVFRGATVCSLDDLDYNGQAKCMLEKVGNNWDFDIFLFDRLT 165

Qy 127 NGNSLVTLCHLNFTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAHAADVQAMH 186
Db 166 NGNSLVSLTFLHLSLGLIETFEHLDVMVKLRRLFLVMIQEDYHSQNPYHNAHAADVQAMH 225

Qy 187 CYLKEPKCLASFLTPDLMGLLAAAHADVDPHPGVNQPFLIKTNHLLANLYQNMSVLENH 246
Db 226 CYLKEPKCLASFLTPDLMGLLAAAHADVDPHPGVNQPFLIKTNHLLANLYQNMSVLENH 285

Qy 247 WRSTTCMLRRESRLLAHLPKX 266
Db 286 WRSVAVGLLRESGLSHLPLE 305

```

## RESULT 11

```

PDE7A_MOUSE
ID PDE7A_MOUSE STANDARD; PRT; 456 AA.
AC P70453; Q9ERB3;

```

SQ SEQUENCE 456 AA; 52442 MW; 0B826B96490D9F6E\_CRC64;  
Query Match 59.3%; Score 913; DB 1; Length 456;  
Best Local Similarity 65.8%; Pred. No. 1.le-74;  
Matches 171; Conservative 36; Mismatches 53; Indels 0; Gaps 0

Qy 7 ERCEILFENPDONAKVCVCMGLDIRLGQTGVRAERGSYPFDIFRLINSTYSGEITGK 66  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
20 KRRGAISYSSDOTALYIRMLGDVRVSRAAGFETERRGSHPYIDFRIFHSQSIEASVSA 79  
Qy : : : : : : : : : : : : : : : : : : : : : : : :  
67 KKVKRLLSFORYFHASFLRGIIPQAPLHLLDDYLGOARHMLSKVGWMDPDIPLFDRLT 126  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
80 RNRRLLSFORLYRSSRVFGATVCCSLDLIDDYNGQAKCMEKVGNWNDFIPLFDRLT 139  
Qy 127 NGNSLVTLCLHFNTGHGLIHFFKLDMVTLHRFLVMVOEDYHSQNPHYNAVAHADVTQAMH 186  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
140 NGNSLSVLTFHLFSLHGELIEFYHLDVMKLRFLVIQEDYHSQNPHYNAVAHADVTQAMH 199  
Qy 187 CYLKKEPKLASFLTPDLTMIGLLAAAHDVDHPGYNQPFLIKTNHHLANLIYQMVSLENHH 246  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
200 CYLKKEPKLASVTPWDITLLSIAAATHLDHPGVNQPFLLIKTNHYLATLYKNSSYLENNH 259  
Qy 247 WRSTIGMRESRLLAHPKE 266  
Db : : : : : : : : : : : : : : : : : : : : : : : :

260 WRSAGVLLREGLFSHLPLE 279

RESULT 12  
Q96T72 HUMAN  
ID Q96T72\_HUMAN PRELIMINARY; PRT; 424 AA.  
AC Q96T72;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC NCBI\_TaxID=9606;  
RN NCBI\_TaxID=9606;  
RX [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=21285467; PubMed=11371644; DOI=10.1073/pnas.101131098;  
RX Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;  
RT "T cell activation up-regulates cyclic nucleotide phosphodiesterases  
8A1 and 7A3";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).  
DR EMBL; AF332852; AK57640.1; -, mRNA.  
DR HSP; Q08499; IOYN.  
DR Ensembl; ENSG00000171408; Homo sapiens.  
DR GO; GO:0004114; F-3'; 5'-cyclic-nucleotide phosphodiesterase a. . ; IEA.  
DR GO; GO:0016787; F-hydrolase activity; IEA.  
DR GO; GO:0007165; p-signal transduction; IEA.  
DR InterPro; IPR03607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDasee.  
DR Pfam; PF00233; PDasee\_1; 1.  
DR PRINTS; PR00387; PDIESTERASE1.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDASEE\_I; UNKNOWN 1.  
SQ SEQUENCE 424 AA; 48627 MW; A7DBF4D008A7B561\_CRC64;

Query Match 58.9%; Score 907; DB 2; Length 424;  
Best Local Similarity 64.6%; Pred. No. 3.5e-74;  
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0

Qy 7 ERCEILFENPDONAKVCVCMGLDIRLGQTGVRAERGSYPFDIFRLINSTYSGEITGK 66  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
46 QRKGAIYSDDOTALYIRMLGDVRVSRAAGFESERGSHPYIDFRIFHSQSIEVSVSA 105  
Qy 67 KKVKRLLSFORYFHASFLRGIIPQAAPLHLLDDYLGOARHMLSKVGWMDPDIPLFDRLT 126  
Db : : : : : : : : : : : : : : : : : : : : : : : :  
106 RNRRLLSFORLYRSSRFGRGTAVSNLTILDDDYGQAKCMEKVGNWNDFIPLFDRLT 165

QY 127 NGNSLVTLCHLFWTHGLIHFKDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186  
 DB 166 NGNSLVSLTFHLPSLHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225  
 QY 187 CYLKEPKLASFLTPDLTLMGLLAAAHDVHPGVNQPFLLKTNHLLANLYQNMSVLENHH 246  
 DB 226 CYLKEPKLANSVTPWDILLSLIAAATHDLDPGVNQPFLLKTNHLLATLYKNTSVLENHH 285  
 QY 247 WRSTIGMLRESRLLAHLKPE 266  
 DB 286 WRSVAVGLLRSGLFSLHPLP 305

RESULT 13  
 PDE7A HUMAN STANDARD; PRT; 482 AA.  
 AC Q13946; Q15380;  
 DT 13-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A  
 DE (EC 3.1.4.17) (HCP1) (TM22).  
 GN Name=PDE7A;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM PDE7A1).  
 RX MEDLINE=93286141; PubMed=839765;  
 RA Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,  
 RA Riggs M., Rodgers L., Beavo J.A., Wigler M.;  
 RT "Isolation and characterization of a previously undetected human cAMP  
 RT phosphodiesterase by complementation of cAMP phosphodiesterase-  
 RT deficient Saccharomyces cerevisiae.";  
 RL J. Biol. Chem. 268:12925-12932(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM PDE7A2).  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=97341143; PubMed=9195912; DOI=10.1074/jbc.272.26.16152;  
 RA Han P., Zhu X., Michaeli T.;  
 RT "Alternative splicing of the high affinity cAMP-specific  
 RT phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";  
 RL J. Biol. Chem. 272:16152-16157(1997).  
 CC -1- FUNCTION: Plays a role in signal transduction by regulating the  
 CC intracellular concentration of cyclic nucleotides. This  
 CC phosphodiesterase is highly specific for cAMP and may have a role  
 CC in muscle signal transduction.  
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =  
 CC adenosine 5'-phosphate.  
 CC -1- COFACTOR: Divalent cations.  
 CC -1- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.  
 CC -1- PATHWAY: Cyclic nucleotide metabolism.  
 CC -1- SUBCELLULAR LOCATION: PDE7A1 (57 kDa) is located mostly to soluble  
 CC cellular fractions. PDE7A2 (50 kDa) is located to particulate  
 CC cellular fractions.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=PDE7A1;  
 CC IsoId=Q13946-1; Sequence=Displayed;  
 CC Name=PDE7A2;  
 CC IsoId=Q13946-2; Sequence=VSP\_004593;  
 CC -1- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal  
 CC muscle and at low levels in a variety of tissues including brain  
 CC and heart. It is expressed as well in two T-cell lines. PDE7A2 is  
 CC found abundantly in skeletal muscle and at low levels in heart.  
 CC -1- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2  
 CC are found in several fetal tissues, expression is reduced  
 CC throughout development. It persists strongly only in adult  
 CC skeletal muscle.  
 CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two  
 CC putative divalent metal sites and an N-terminal regulatory domain.

CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
 CC family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR ENBL; L12052; AAA35644.2; -; mRNA.  
 DR ENBL; U67932; AAB65772.1; -; mRNA.  
 DR HSSP; Q08499; IOYN.  
 DR HGNC; HGNC:8791; PDE7A.  
 DR MIM; 171885; -;  
 DR GO; GO:0000267; C-cell fraction; NAS.  
 DR GO; GO:0004115; P: cAMP-specific phosphodiesterase activity; TAS.  
 DR GO; GO:0007165; P: signal transduction; NAS.  
 DR InterPro; IPR002073; PDEase.  
 DR Pfam; PF00233; PDEase I; 1.  
 DR PRINTS; PR00387; PD1ESTERASE1.  
 DR PROSITE; PS00126; PDEASE\_1; 1.  
 KW Alternative splicing; cAMP; Hydrolase; Phosphorylation.  
 FT REGION 187 451  
 FT COMPBIAS 28 33 Poly-Ser.  
 FT MOD RES 84 84 Phosphoserine (Potential).  
 FT VARSPLIC 1 46 MEVCYQLPVLPLDRPVPQHVLSRRGALSRSSSSALFGCPNP  
 FT RQLSQ -> MGI TLWCLALVLKWTISK (in isoform  
 FT PDE7A2).  
 FT /FTID=VSP\_004593.  
 SQ SEQUENCE 482 AA; 55505 MW; 3B3C8F6E9154F88C CRC64;  
 Query Match 58.9%; Score 907; DB 1; Length 482;  
 Best Local Similarity 64.6%; Pred. No. 4.1e-74;  
 Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;  
 QY 7 ERCEILFENPDQNAKVCVCMGLGDIRLRGTGVRAERRSGSYPPDFRLNLTYSYSGIGTK 66  
 DB 46 QRRGALSYDSSDQALYIRMLGDVVRVRSRAGFESERRGSHPYIDFRIFHSQSIEVSVA 105  
 QY 67 KVKVRLLSFQRYFHASRLRGLIIPQAPLHLLDEDYLGQARHMLSKYGMWDFDIFLDRLT 126  
 DB 106 RNIIRLLSFQRYLRSRFRFTAVNSNLILDDYNGQAKMLEKVGNNWDFDIFLDRLT 165  
 QY 127 NGNSLVTLCHLFWTHGLIHFKDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186  
 DB 166 NGNSLVSLTFHLPSLHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225  
 QY 187 CYLKEPKLASFLTPDLTLMGLLAAAHDVHPGVNQPFLLKTNHLLANLYQNMSVLENHH 246  
 DB 226 CYLKEPKLANSVTPWDILLSLIAAATHDLDPGVNQPFLLKTNHLLATLYKNTSVLENHH 285  
 QY 247 WRSTIGMLRESRLLAHLKPE 266  
 DB 286 WRSVAVGLLRSGLFSLHPLP 305

RESULT 14  
 QSR5B5 PONPY PRELIMINARY; PRT; 456 AA.  
 AC QSR5B5;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DE Hypothetical protein DKFZp469E1731.  
 GN Name=DKFZp469E1731;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Pongo.  
 OC NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;

Search completed: March 10, 2006, 20:02:06  
Job time : 124.195 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:02:25 ; Search time 26.1463 Seconds  
(without alignments)  
910.666 Million cell updates/sec

Title: US-10-781-181-3  
Perfect score: 1540  
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLDRLTNGNSLV 288

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	83.1	320	2	US-09-330-970-3
2	1280	83.1	502	2	US-09-330-970-1
3	1073	69.7	390	2	US-09-949-016-10020
4	907	58.9	498	1	US-07-688-352C-20
5	907	58.9	498	1	US-08-474-379C-20
6	907	58.9	498	2	US-09-146-249A-20
7	907	58.9	498	2	US-08-206-188B-20
8	331.5	21.5	517	2	US-09-602-735B-4
9	330.5	21.5	451	1	US-08-474-379C-61
10	330.5	21.5	451	2	US-09-146-249A-61
11	330.5	21.5	451	2	US-08-206-188B-61
12	330.5	21.5	518	2	US-09-602-735B-2
13	330.5	21.5	673	1	US-08-577-492-35
14	330.5	21.5	673	1	US-08-474-379C-63
15	330.5	21.5	673	2	US-09-146-249A-63
16	330.5	21.5	673	2	US-08-206-188B-63
17	330.5	21.5	673	2	US-09-079-630-35
18	323	21.0	302	4	PCT-US91-02714-21
19	323	21.0	398	1	US-08-474-379C-86
20	323	21.0	638	1	US-07-688-352C-22
21	323	21.0	734	2	US-09-146-249A-85
22	323	21.0	734	2	US-08-206-188B-85
23	320.5	20.8	686	1	US-08-942-521B-9
24	320.5	20.8	885	1	US-08-577-492-33
25	320.5	20.8	885	2	US-09-079-630-33
26	320.5	20.8	886	2	US-08-474-379C-65
27	320.5	20.8	886	2	US-09-146-249A-65

28 320.5 20.8 886 2 US-08-206-188B-65 Sequence 65, Appl  
29 320.5 20.8 901 2 US-09-917-254-93 Sequence 93, Appl  
30 318.5 20.7 721 2 US-09-983-754-2 Sequence 2, Appl  
31 317.5 20.6 562 1 US-07-688-352C-4 Sequence 4, Appl  
32 317.5 20.6 562 1 US-08-942-521B-8 Sequence 8, Appl  
33 317.5 20.6 562 1 US-08-474-379C-4 Sequence 4, Appl  
34 317.5 20.6 562 1 US-09-146-249A-4 Sequence 4, Appl  
35 317.5 20.6 562 2 US-08-206-188B-4 Sequence 4, Appl  
36 317.5 20.6 562 4 PCT-US91-02714-4 Sequence 4, Appl  
37 316.5 20.6 610 1 US-08-974-565C-9 Sequence 9, Appl  
38 316.5 20.6 610 2 US-09-255-748-9 Sequence 34, Appl  
39 314.5 20.4 564 1 US-08-577-492-34 Sequence 2, Appl  
40 314.5 20.4 564 1 US-08-942-521B-2 Sequence 2, Appl  
41 314.5 20.4 564 1 US-08-474-379C-59 Sequence 59, Appl  
42 314.5 20.4 564 2 US-09-146-249A-59 Sequence 59, Appl  
43 314.5 20.4 564 2 US-08-206-188B-59 Sequence 59, Appl  
44 314.5 20.4 564 2 US-09-192-702-2 Sequence 2, Appl  
45 314.5 20.4 564 2 US-09-079-630-34 Sequence 34, Appl

## ALIGNMENTS

RESULT 1  
US-09-330-970-3  
; Sequence 3, Application US/09330970  
; Patent No. 6146876  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: White, David  
; TITLE OF INVENTION: A NO. 6146876el Human Cyclic Nucleotide  
; FILE OF INVENTION: Phosphodiesterase  
; FILE REFERENCE: 5800-28  
; CURRENT APPLICATION NUMBER: US/09/330,970  
; CURRENT FILING DATE: 1999-06-11  
; EARLIER APPLICATION NUMBER: 09/277,423  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-330-970-3

Query Match 83.1%; Score 1280; DB 2; Length 320;  
Best Local Similarity 100.0%; Pred. No. 3.8e-140; Mismatches 0; Gaps 0;  
Matches 241; Conservative 0; Indels 0;  
Qy 28 GDILRGQTGVRAERGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87  
Db 80 GDILRGQTGVRAERGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139  
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 199  
Qy 148 FKLDWTLHRLFLVMVQSDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMGL 207  
Db 200 FKLDWTLHRLFLVMVQSDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMGL 259  
Qy 208 LAAAAHDVHPGYNQPFLLIKTNHHLANLYQNMVLENHHRSTIGMLRESLLAHLPKEM 267  
Db 260 LAAAAHDVHPGYNQPFLLIKTNHHLANLYQNMVLENHHRSTIGMLRESLLAHLPKEM 319  
Qy 268 T 268  
Db 320 T 320  
RESULT 2  
US-09-330-970-1

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; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-1

Query Match      83.1%; Score 1280; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 7.4e-140;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDRLRGOTGVRAERRGSGYFIDFRLNLTSTYSGEIGTKKKVKRLLSQRYFHASRLRG 87
Db 80 GDRLRGOTGVRAERRGSGYFIDFRLNLTSTYSGEIGTKKKVKRLLSQRYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 147
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 207
Db 200 FKLDMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 259

Qy 208 LAAAHVDVHPGVNQPLIKTNHHLNLYQNMVLENHHWRSTIGMLRESLLAHLPKEM 267
Db 260 LAAAHVDVHPGVNQPLIKTNHHLNLYQNMVLENHHWRSTIGMLRESLLAHLPKEM 319

Qy 268 T 268
Db 320 T 320

RESULT 3
US-09-949-016-10020
; Sequence 10020, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10020
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10020

Query Match      69.7%; Score 1073; DB 2; Length 390;
Best Local Similarity 86.7%; Pred. No. 6.1e-116;

; Sequence 1, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-688-352C-20

Query Match      58.9%; Score 907; DB 1; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Qy 29 DIHLRGOTGVRAERRGSGYFIDFRLNLTSTYSGEIGTKKKVKRLLSQRYFHASRLRG 88
Db 1 DIHLRGOTGVRAERRGSGYFIDFRLNLTSTYSGEIGTKKKVKRLLSQRYFHASRLRG 60

Qy 89 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHH 148
Db 61 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTN----- 99

Qy 149 KLDMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 208
Db 100 -----VVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 148

Qy 209 AAAAAVDVHPGVNQPLIKTNHHLNLYQNMVLENHHWRSTIGMLRESLLAHLPKEM 268
Db 149 AAAAAVDVHPGVNQPLIKTNHHLNLYQNMVLENHHWRSTIGMLRESLLAHLPKEM 208

RESULT 4
US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-688-352C-20

Query Match      58.9%; Score 907; DB 1; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Qy 7 ERGCEILFENPDONAKVCVCMGLDIRLGTQGVRAERRGSGYFIDFRLNLTSTYSGEIGTK 66
Db 62 QRRGAIYDSSDQALYIRMLGDIVRVRSGPESERRGSHPYIDFRIFHSQSEIEVSVA 121
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7 ERCGEILFENPDQNAKVCMLGDIRLRGOTGVRAERRGSYPFFIDFRLNLTYSGEIGTK 66

Qy	7	ERCGEILFENDPONAKVCMLGDRI LRGTGVRAERRGSYPTDFRLLNSTTYSGEIGTK	66
Db	62	ORRGATSYSDSOTALYIRMLGDVVRVSRRAGFESESRGSHPYDIFRIFHSOSIEVSVSA	121



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; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-379C-61

Query Match 21.5%; Score 330.5; DB 1; Length 451;
Best Local Similarity 37.8%; Pred. No. 1.8e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS-----PQRYFHASRLRLGIIPQAPLHLLDEYLGQARHMLSKVGWMDFIPL 121
Db 234 KKKKRPMSQISGVKKLMHSSSLTNSIPRGVKTQEDVLAK-----LEDVKNKGLHVR 290

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDVMTLHRLFLVMQVDYHSQNPYHNAHAAD 180
Db 291 IAEI-SGNRPLTVIMHTIFQERDLTKTKIPVDLTLYLMTLEDHYHADVAYHNNIHAAD 349

Qy 181 VTQAMHCYKLEPKLASPLTDLIMGLLAAAHAHDVDPHGYNQPELIKTNHHLNLYQNS 240
Db 350 VQSTHVLSTPALEAVFTDLLEILAAIFASAIHDVDHPGVSNQPLINTNSELALMYNDSS 409

Qy 241 VLENHWRSTIGMLRE 256
Db 410 VLENHHLAVGFKLIQE 425

RESULT 10
US-09-146-249A-61
; Sequence 61, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994

Query Match 21.5%; Score 330.5; DB 2; Length 451;
Best Local Similarity 37.8%; Pred. No. 1.8e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS-----PQRYFHASRLRLGIIPQAPLHLLDEYLGQARHMLSKVGWMDFIPL 121
Db 234 KKKKRPMSQISGVKKLMHSSSLTNSIPRGVKTQEDVLAK-----LEDVKNKGLHVR 290

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDVMTLHRLFLVMQVDYHSQNPYHNAHAAD 180
Db 291 IAEI-SGNRPLTVIMHTIFQERDLTKTKIPVDLTLYLMTLEDHYHADVAYHNNIHAAD 349

Qy 181 VTQAMHCYKLEPKLASPLTDLIMGLLAAAHAHDVDPHGYNQPELIKTNHHLNLYQNS 240
Db 350 VQSTHVLSTPALEAVFTDLLEILAAIFASAIHDVDHPGVSNQPLINTNSELALMYNDSS 409

Qy 241 VLENHWRSTIGMLRE 256
Db 410 VLENHHLAVGFKLIQE 425

RESULT 11
US-08-206-188B-61
; Sequence 61, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-206-188B-61

Query Match      21.5%; Score 330.5; DB 2; Length 451;
Best Local Similarity 37.8%; Pred. No. 1.8e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS---FQRYFHASRLLRGIIPOAPLHLLDEYVGOARHMLSKVGMWDFDIFL 121
Db 234 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTQEDVLAKE---LEDVNWKGLHVR 290

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMQEDYHSQNPYHNAHAAD 180
Db 291 IABL-SGNRPLTVIMHTIFQERDLLTKFKIPVDTLITLTYLMTLEDHYHADVAYHNNIHAAD 349

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHADVDPGVNQPFLLIKTNHHLANLYONMS 240
Db 350 VQSTHVLSTPALEAVFTDLILAAIFASAIHDVDPGVNQPFLLIKTNHHLANLYONMS 240

Qy 241 VLENHHWRSTIGMLRE 256
Db 410 VLENHHLAVGFKLQE 425

RESULT 12
US-09-602-735B-2
; Sequence 2, Application US/09602735B
; Patent No. 6656717
; GENERAL INFORMATION:
; APPLICANT: Xln, Xiaonan
; APPLICANT: Unterbeck, Axel
; APPLICANT: Hu, Yinghe
; TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
; FILE REFERENCE: Use
; FILE REFERENCE: 453260-55
; CURRENT APPLICATION NUMBER: US/09/602,735B
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/141,196
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-602-735B-2

Query Match      21.5%; Score 330.5; DB 2; Length 518;
Best Local Similarity 37.8%; Pred. No. 2.2e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS---FQRYFHASRLLRGIIPOAPLHLLDEYVGOARHMLSKVGMWDFDIFL 121
Db 63 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTQEDVLAKE---LEDVNWKGLHVR 119

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMQEDYHSQNPYHNAHAAD 180
Db 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMQEDYHSQNPYHNAHAAD 180

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/577,492
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Owens, Raymond John
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-08-577-492-35

Query Match      21.5%; Score 330.5; DB 1; Length 673;
Best Local Similarity 37.8%; Pred. No. 3.3e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS---FQRYFHASRLLRGIIPOAPLHLLDEYVGOARHMLSKVGMWDFDIFL 121
Db 218 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTQEDVLAKE---LEDVNWKGLHVR 274

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMQEDYHSQNPYHNAHAAD 180
Db 275 IABL-SGNRPLTVIMHTIFQERDLLTKFKIPVDTLITLTYLMTLEDHYHADVAYHNNIHAAD 333

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHADVDPGVNQPFLLIKTNHHLANLYONMS 240
Db 334 VQSTHVLSTPALEAVFTDLILAAIFASAIHDVDPGVNQPFLLIKTNHHLANLYONMS 393
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Qy	241	VLENHWRSTIGMLRE	256
			:
Db	394	VLENHHLAVGFKLLOE	409

RESULT 14  
US-08-474-379C-63  
; Sequence 63, Application US/08474379C  
; Patent No. 5977305  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
; TITLE OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,379C  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/206,188  
; FILING DATE: 01-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,352  
; FILING DATE: 19-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 27866/32771  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-379C-63

Query Match	21.5%	Score 330.5	DB 1	Length 673
Best Local Similarity	37.8%	Pred. No. 3.3e-29		
Matches	74	Conservative 35	Mismatches 78	Indels 9
Gaps	4			
Qy	66	KKGVKRLLS----	FQRYFHASRLRGIGIPQAPLHLLDE	DYILGQARHMLSKVGMWDFOIFL 121
Db	218	KEKKRPMISQISGVKLMHSSLTNS	SIPRGVKTQEDVLAK---	LEDVNKMGILHVF 274
Qy	122	FDRLTNGNSLVTLTCH--	LENTHGLIHFFKLDVMVTLH	FLVMVQSDYHSQNPYHNAVAAD 180
Db	275	IAEL--SGNRPLTVIMHTYIFQER	DLTKFKIPVDTLITYLTLED	HDYHADVAYHNNIHAAD 333
Qy	181	VTQAMHCYLPKPKASLFTPLD	IMGLLAAAHHVDHPGVNQ	PPFLTKTNHHLANLYQMS 240
Db	334	VWOSTHYLLSTPALEAVFTOLE	LAIPAFAIAHVDVHPGVSNQ	PLINTNSSELALMYNDSS 393
Qy	241	VLENHHWRSTIGMLRE 256		

394 VLENHHLAVCFKLQZ 409

RESULT 15  
US-09-146-249A-63  
Sequence 63, Application US/09146249A  
Patent No. 6069240  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Co  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, G  
STREET: 6300 Sears Tower, 233 S  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of Ameri  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,2,2  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,7  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-146-249A-63

Query Match	21.5%	Score 330.5;	DB 2;	Length 673;
Best Local Similarity	37.8%;	Pred. No. 3.3e-29;		
Matches	74;	Conservative 35;	Mismatches 78;	Indels 9; Gaps 4;
Qy	66	KKVKKLLS----	FORVFHASRLRGII	POAPLHLLDDEDYLGQARHMSKVGWMDFOIFL 121
Db	218	KEKKKPMQISGVKKLMSSSLTNSIS	PRFGVKTQEDVLAK----	LEDVKNWGLHVF 274
Qy	122	FDRLTNGNSLVTL	LCH-LFNTHGLIHFKLDVMYTLHRFLV	WQEDYHSQNPYHNAVAAD 180
Db	275	IABL-SGNRLTVIMHT	IFOERDLKTKFPVDTLITYLMTLED	HDYHADVAYHNNIHAAD 333
Qy	181	VTQAMCHYLKEPKLASFL	PLDTIMGLGAAAAHDVHPGVNQDFL	IKTNHHLANLYONMS 240
Db	334	VQSTVLLSTPALEAVFTD	LEITAAIFASIHVDVHPGVNQFLINTN	SELALMYNDSS 393
Qy	241	VLENHHWRSTIGMLRE	256	
Db	394	VLENHHAVGFKLLOE	409	

Search completed: March 10, 2006, 20:04:13  
Job time : 27.1463 secs

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# OM protein - protein search, using sw model

Run on: March 10, 2006, 20:18:07 ; Search time 87.0244 Seconds  
(without alignments)  
1382.771 Million cell updates/sec

Title: US-10-781-181-3  
Perfect score: 1540  
Sequence: 1 MSLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	288	4	US-10-781-181-3
2	1430	92.9	450	4	US-10-781-181-5
3	1430	92.9	450	5	US-10-284-268A-2
4	1376	89.4	446	4	US-10-781-181-1
5	1280	83.1	320	4	US-10-386-414-6
6	1280	83.1	502	4	US-10-273-517-1
7	1280	83.1	502	4	US-10-386-414-4
8	1280	83.1	502	4	US-10-311-104-1
9	1280	83.1	502	6	US-11-048-744-1
10	1280	83.1	502	6	US-11-048-068-1
11	1145	74.4	391	5	US-10-204-268A-4
12	980	63.6	335	5	US-10-771-833-23
13	980	63.6	335	5	US-10-886-949-23
14	907	58.9	424	5	US-10-380-437-6
15	907	58.9	424	5	US-10-380-437-53
16	907	58.9	432	3	US-09-764-898-208
17	898	58.3	426	3	US-09-966-781A-2
18	892	57.9	426	3	US-09-966-781A-3
19	891	57.9	426	3	US-09-966-781A-1
20	725	47.1	334	5	US-10-771-833-22
21	725	47.1	334	5	US-10-886-949-22
22	682	44.3	336	4	US-10-258-746-2
23	531	34.5	99	4	US-10-781-181-16
24	392	25.5	211	3	US-09-764-898-280
25	392	25.5	211	3	US-09-989-442-120
26	331.5	21.5	517	4	US-10-682-722-4
27	331.5	21.5	747	5	US-10-492-835-8

28	331.5	21.5	747	5	US-10-492-835-15	Sequence 15, Appl
29	331.5	21.5	747	5	US-10-492-835-27	Sequence 27, Appl
30	330.5	21.5	507	4	US-10-076-597-49	Sequence 49, Appl
31	330.5	21.5	507	4	US-10-067-514-10	Sequence 10, Appl
32	330.5	21.5	507	4	US-10-419-723-10	Sequence 10, Appl
33	330.5	21.5	507	4	US-10-255-120-10	Sequence 10, Appl
34	330.5	21.5	507	4	US-10-755-889-304	Sequence 304, App
35	330.5	21.5	507	5	US-10-868-397-10	Sequence 10, Appl
36	330.5	21.5	518	4	US-10-682-722-2	Sequence 2, Appli
37	330.5	21.5	585	4	US-10-067-514-9	Sequence 9, Appli
38	330.5	21.5	585	4	US-10-419-723-9	Sequence 9, Appli
39	330.5	21.5	585	4	US-10-255-120-9	Sequence 9, Appli
40	330.5	21.5	585	5	US-10-868-397-9	Sequence 9, Appli
41	330.5	21.5	664	5	US-10-735-973-2	Sequence 2, Appli
42	330.5	21.5	673	4	US-10-076-597-51	Sequence 51, Appli
43	330.5	21.5	673	4	US-10-067-514-6	Sequence 6, Appli
44	330.5	21.5	673	4	US-10-419-723-6	Sequence 6, Appli
45	330.5	21.5	673	4	US-10-255-120-6	Sequence 6, Appli

## ALIGNMENTS

### RESULT 1

US-10-781-181-3  
; Sequence 3, Application US/10781181  
; Publication No. US20040137508A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Fiddock, Mark David  
; TITLE OF INVENTION: Enzyme PDE xiv  
; FILE REFERENCE: PC10315B  
; CURRENT APPLICATION NUMBER: US/10/781,181  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: GB 9828603.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 09/471,459  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: GB 9922123.6  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Human  
US-10-781-181-3

Query Match 100.0%; Score 1540; DB 4; Length 288;  
Best Local Similarity 100.0%; Pred. No. 3e-154;  
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTVRAERGSYPFIDFRLNLTYS 60  
Db 1 MSLMVERCGEILFENPDQNAKVCMLGDIRLRGQTVRAERGSYPFIDFRLNLTYS 60  
QY 61 GEIGTKKKVKRLLSFQRYFHASRLRGITPQAPLHLLDELDYLGQARHLSKVGWDFDIF 120  
Db 61 GEIGTKKKVKRLLSFQRYFHASRLRGITPQAPLHLLDELDYLGQARHLSKVGWDFDIF 120  
QY 121 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMQEDYHSQNPYHNAVAAD 180  
Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMQEDYHSQNPYHNAVAAD 180  
QY 181 VTQAMCHYLKEPKLASFLPLDLMGLAAAADVDHPGVNQPFLLKTNHHLANLYQMS 240  
Db 181 VTQAMCHYLKEPKLASFLPLDLMGLAAAADVDHPGVNQPFLLKTNHHLANLYQMS 240  
QY 241 VLENHHRSTIGMLRESRLIAHLPKMTGTWDFDIFLFDRLTNGNSLV 288  
Db 241 VLENHHRSTIGMLRESRLIAHLPKMTGTWDFDIFLFDRLTNGNSLV 288

```
RESULT 2
US-10-781-181-5
; Sequence 5, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: Enzyme PDE xiv
; FILE REFERENCE: PC10315B
; CURRENT APPLICATION NUMBER: US/10/781.181
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: GB 9828603.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/471,459
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 9922123.6
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Human
US-10-781-181-5

Query Match      92.9%; Score 1430; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.5e-142;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Db 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Qy 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Db 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Qy 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
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RESULT 3
US-10-204-268A-2
; Sequence 2, Application US/10204268A
; Publication No. US2005058647A1
; GENERAL INFORMATION:
; APPLICANT: KLUXEN, FRANZ-WERNER
; APPLICANT: HENTSCH, BERND
; TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
; FILE REFERENCE: MERCK-2484
; CURRENT APPLICATION NUMBER: US/10/204, 268A
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/EP01/01858
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: EP 00103655.7
; PRIOR FILING DATE: 2000-02-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-204-268A-2
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Query Match      92.9%; Score 1430; DB 5; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.5e-142;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Db 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Qy 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Db 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Qy 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268

RESULT 4
US-10-781-181-1
; Sequence 1, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: Enzyme PDE xiv
; FILE REFERENCE: PC10315B
; CURRENT APPLICATION NUMBER: US/10/781.181
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: GB 9828603.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/471,459
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 9922123.6
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Mouse
US-10-781-181-1

Query Match      89.4%; Score 1376; DB 4; Length 446;
Best Local Similarity 95.1%; Pred. No. 1.3e-136;
Matches 255; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Db 1 MSCLMVERCGEILFENPDQNAKVCMLGDIRLGRGQTGVRAERRGSYFFIDFRLNLTYS 60
Qy 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Db 61 GEIGTKKKVKRLLSFORYPFASRLRGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIF 120
Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWMTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
Qy 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
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RESULT 5  
US-10-386-414-6  
; Sequence 6, Application US/10386414  
; Publication No. US20040006016A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; FILE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MPI03-0210MNM  
; CURRENT APPLICATION NUMBER: US/10/386,414  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: 09/426,282  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 09/668,266  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/330,970  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: 09/724,599  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/860,193  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 10/283,023  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/010,943  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 60/254,037  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/833,082  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-386-414-6  
Query Match 83.1%; Score 1280; DB 4; Length 320;  
Best Local Similarity 100.0%; Pred. No. 1.2e-126;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GDRLRGQTGVRAERGSYPFDRLNLSNNTYSGEIGTKKKVKLLSFGQYFHASRLRG 87  
DB 80 GDRLRGQTGVRAERGSYPFDRLNLSNNTYSGEIGTKKKVKLLSFGQYFHASRLRG 139  
QY 88 IIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
DB 140 IIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199  
QY 148 FKLDVMTLHRLVLMVQEDYHSQNPYHNAHAADVTQAMHCYKLPKSLASFLTPDLMGL 207  
DB 200 FKLDVMTLHRLVLMVQEDYHSQNPYHNAHAADVTQAMHCYKLPKSLASFLTPDLMGL 259  
QY 208 LAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 267  
DB 260 LAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 319  
QY 268 T 268  
DB 320 T 320

RESULT 6  
US-10-273-517-1  
; Sequence 1, Application US/10273517  
; Publication No. US20030143588A1  
; GENERAL INFORMATION:  
; APPLICANT: THORNTON, Michael B.; DING, Li  
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.  
; APPLICANT: TRIBOULEY, Catherine M.; LAU, Preeti G.  
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.  
; APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan  
; APPLICANT: CHAWLA, Narinder K.  
; TITLE OF INVENTION: PHOSPHODIESTERASES  
; FILE REFERENCE: PI-0136 USA  
; CURRENT APPLICATION NUMBER: US/10/273,517  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 60/241,100  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/218,234  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US01/20140  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/213,741  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1  
US-10-273-517-1  
Query Match 83.1%; Score 1280; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 2.3e-126;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GDRLRGQTGVRAERGSYPFDRLNLSNNTYSGEIGTKKKVKLLSFGQYFHASRLRG 87  
DB 80 GDRLRGQTGVRAERGSYPFDRLNLSNNTYSGEIGTKKKVKLLSFGQYFHASRLRG 139  
QY 88 IIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
DB 140 IIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199  
QY 148 FKLDVMTLHRLVLMVQEDYHSQNPYHNAHAADVTQAMHCYKLPKSLASFLTPDLMGL 207  
DB 200 FKLDVMTLHRLVLMVQEDYHSQNPYHNAHAADVTQAMHCYKLPKSLASFLTPDLMGL 259  
QY 208 LAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 267  
DB 260 LAAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHRSTIGMLRESRLLAHLPKEM 319  
QY 268 T 268  
DB 320 T 320

RESULT 7  
US-10-386-414-4  
; Sequence 4, Application US/10386414  
; Publication No. US20040006016A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.

```
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-4

Query Match      83.1%; Score 1280; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDRLRGQTGVRAERGSYPFDIFRLNLSNTTYSGEIGTKKKVRLLSFQRYFHASRLRG 87
Db 80 GDRLRGQTGVRAERGSYPFDIFRLNLSNTTYSGEIGTKKKVRLLSFQRYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 207
Db 200 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 259

Qy 208 LAAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
Db 260 LAAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy 268 T 268
Db 320 T 320

RESULT 8
US-10-311-104-1
; Sequence 1, Application US/10311104
; Publication No. US20040054138A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: THORNTON, Michael
; APPLICANT: DING, Li
; APPLICANT: ARVIZU Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: HAFALIA, April J. A.
; APPLICANT: BAUGHN, Mariah R.

Query Match      83.1%; Score 1280; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDRLRGQTGVRAERGSYPFDIFRLNLSNTTYSGEIGTKKKVRLLSFQRYFHASRLRG 87
Db 80 GDRLRGQTGVRAERGSYPFDIFRLNLSNTTYSGEIGTKKKVRLLSFQRYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 207
Db 200 FKLDVMTLHRLVWQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 259

Qy 208 LAAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
Db 260 LAAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy 268 T 268
Db 320 T 320

RESULT 9
US-11-048-744-1
; Sequence 1, Application US/11048744
; Publication No. US20050164275A1
; GENERAL INFORMATION:
; APPLICANT: THORNTON, Michael B.; DING, Li
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.
; APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan
; APPLICANT: CHAWLA, Narinder K.
; TITLE OF INVENTION: PHOSPHODIESTERASES
; FILE REFERENCE: PI-0136 USA
; CURRENT APPLICATION NUMBER: US/11/048,744
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: US/10/273,517
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/241,100
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/218,234
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US01/20140
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; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 7476201CD1  
 US-11-048-068-1

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Db 190 LANLYQNSVLENHHWRSTIGMLRESRLLAHLPKMT 226
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RESULT 12
US-10-771-833-23
; Sequence 23, Application US/10771833
; Publication No. US20050048573A1
; GENERAL INFORMATION:
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: PDESA CRYSTAL STRUCTURE AND USES
; FILE REFERENCE: 039363-1106
; CURRENT APPLICATION NUMBER: US/10/771.833
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: 60/444,734
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-833-23

Query Match 63.6%; Score 980; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 7.9e-95;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIH 146
Db 1 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIH 60
|||||

Qy 147 HFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDMLG 206
Db 61 HFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDMLG 120
|||||

Qy 207 LLA AAAHDVDPHGVNPFLLKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 266
Db 121 LLA AAAHDVDPHGVNPFLLKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 180
|||||

Qy 267 MT 268
||
Db 181 MT 182

RESULT 14
US-10-380-437-6
; Sequence 6, Application US/10380437
; Publication No. US20050058998A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A
; APPLICANT: Seebek, Thomas
; APPLICANT: Soderling, Scott Haydn
; APPLICANT: Rascon, Ana
; APPLICANT: Zoraghi, Roya
; APPLICANT: Kunz, Stefan
; APPLICANT: Gong, Kewei
; APPLICANT: Glavas, Natalie
; TITLE OF INVENTION: NOVEL PDES AND USES THEREOF
; FILE REFERENCE: 30429.3W001
; CURRENT APPLICATION NUMBER: US/10/380,437
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/232,445
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/240,500
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-437-6

Query Match 58.9%; Score 907; DB 5; Length 424;
Best Local Similarity 64.6%; Pred. No. 5.9e-87;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Qy 7 ERCGEILFENPDQNAKVCMLGDIRLGTQVRAERGRSYPFIDFRLNSTYSGBIGTK 66
Db 46 QRRGALSVDSDQALYIRMLGDVVRVRAGFESERRGSHPIDRIFHSQSIEVSVA 105
|||||

Qy 67 KVKRLLSPQRYPHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLT 126
Db 106 RNIRLLSPQRYLRSSRFRGTAVSNSILDDVNGQAKCMLEKVGNNWDFDIFLFDRLT 165
|||||

Qy 127 NGNSLVTLCHLFNTHGLIHHEPKLDMVTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMH 186
Db 166 NGNSLVTLCHLFNTHGLIHHEPKLDMVTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMH 225
|||||

Qy 187 CYLKEPKLASFLTPDMLGLLAAAADVDHFGVNPFFLKTNNHHLANLYQNMSVLENHH 246
Db 226 CYLKEPKLASVTPWDILLSLAAATHDLDFGVNQPFLKTNNHLYLATLYKNTSVLENHH 285
|||||

Qy 247 WRSTIGMLRESRLLAHLPK 266
||
Db 286 WRSVGLLRSGLSHLPLE 305

Query Match 63.6%; Score 980; DB 5; Length 335;
US-10-886-949-23
; Sequence 23, Application US/10886949
; Publication No. US20050079548A1
; GENERAL INFORMATION:
; APPLICANT: DEAN R. ARTIS
; APPLICANT: BOLLAG, GIDRON
; APPLICANT: CARD, GRAHAM
; APPLICANT: MARTIN, FERNANDO
; APPLICANT: MILBURN, MICHAEL V.
; APPLICANT: ZHANG, KAM
; TITLE OF INVENTION: PDESA CRYSTAL STRUCTURE AND USES
; FILE REFERENCE: 039363-1108
; CURRENT APPLICATION NUMBER: US/10/886,949
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-949-23
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## RESULT 15

US-10-380-437-53  
; Sequence 53, Application US/10380437  
; Publication No. US20050058998A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A  
; APPLICANT: Seebeck, Thomas  
; APPLICANT: Soderling, Scott Haydn  
; APPLICANT: Rascon, Ana  
; APPLICANT: Zoraghi, Roya  
; APPLICANT: Kunz, Stefan  
; APPLICANT: Gong, Kewei  
; APPLICANT: Glavas, Natalie  
; TITLE OF INVENTION: NOVEL PDES AND USES THEREOF  
; FILE REFERENCE: 30429.3W001  
; CURRENT APPLICATION NUMBER: US/10/380,437  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: 60/232,445  
; PRIOR FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/240,500  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-380-437-53

Query Match 58.9%; Score 907; DB 5; Length 424;  
Best Local Similarity 64.6%; Pred. No. 5.9e-87;  
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Qy	7	ERCEILFENPDQNAKCVCMGLDIRLGGTVRAERGSYPFIDFRLNLTYSGEIGTK	66
Db	46	ORGAISYDSDQTALYIRMLGTVRVRSRAGFSEERGSHPYIDFRIFHSQSIEVSVA	105
Qy	67	KKVKRLLSQRYPHASRLRLGIIPQAPLHLLDELDYLQARHMLSKVGMWDFDIFLFDRLT	126
Db	106	RNIRRLLSFQYLRSSRFRFGTAVSNSLNILDDDDYNGQAKCMLEKVGWNFDIFLFDRLT	165
Qy	127	NGNSLVTLCHLFTNTHGLIHFKLDWVTLHRFLVMQEDYHSONPYHNAVHAADVTQAMH	186
Db	166	NGNSLVSLTFHLSHGLIEYFHLDMKLRFLVMIQEDYHSONPYHNAVHAADVTQAMH	225
Qy	187	CYLKEPKLASFLPTDLMGLAAAHVDVDPGVNQPFLLKTNHHLANLYONMSVLENHH	246
Db	226	CYLKEPKLANSVTPWDILLSLIAAAHDLDPGVNQPFLLKTNHHLATLYKNTSVLENHH	285
Qy	247	WRSTIGMLRESRLLAHLPE	266
Db	286	WRSVGLLRRESGLFSLPLE	305

Search completed: March 10, 2006, 20:22:33  
Job time : 88.0244 secs

**This Page Blank (uspio)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:19:01 ; Search time 11.3171 Seconds  
(without alignments)  
708.350 Million cell updates/sec

Title: US-10-781-181-3

Perfect score: 1540

Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGSLV 288

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1280	83.1	320	7	US-11-226-701-6
2	1280	83.1	502	7	US-11-226-701-4
3	331.5	21.5	747	6	US-10-492-835-8
4	331.5	21.5	747	6	US-10-492-835-15
5	331.5	21.5	747	6	US-10-492-835-27
6	330.5	21.5	507	7	US-11-091-018-10
7	330.5	21.5	585	7	US-11-091-018-9
8	330.5	21.5	673	7	US-11-091-018-6
9	330.5	21.5	687	7	US-11-091-018-8
10	330.5	21.5	745	7	US-11-091-018-4
11	330.5	21.5	748	6	US-10-492-835-12
12	330.5	21.5	748	6	US-10-492-835-28
13	330.5	21.5	809	7	US-11-091-018-2
14	314.5	20.4	736	7	US-11-169-041-207
15	303.5	19.7	398	7	US-11-123-893-11
16	302.5	19.6	349	7	US-11-123-893-13
17	286.5	19.3	357	7	US-11-123-893-12
18	261	16.9	769	7	US-11-072-512-2646
19	189	12.3	786	6	US-11-072-512-2944
20	185	12.0	941	6	US-10-501-035-343
21	176.5	11.5	854	6	US-10-511-657-4
22	98	6.4	968	6	US-10-501-035-219
23	84	5.5	635	7	US-11-096-568A-29628
24	84	5.5	710	7	US-11-096-568A-29627
25	82.5	5.4	418	7	US-11-109-156-2

Sequence 5451, Ap  
Sequence 5004, Ap  
Sequence 56, Appl  
Sequence 10379, A  
Sequence 27797, A  
Sequence 1, Appli  
Sequence 988, App  
Sequence 5912, Ap  
Sequence 61, Appl  
Sequence 1516, Ap  
Sequence 4038, Ap  
Sequence 4756, Ap  
Sequence 8044, Ap  
Sequence 8917, Ap  
Sequence 735, App  
Sequence 12387, A  
Sequence 12386, A  
Sequence 27808, A  
Sequence 7032, Ap  
Sequence 7719, Ap

#### ALIGNMENTS

#### RESULT 1

US-11-226-701-6  
; Sequence 6, Application US/11226701  
; Publication No. US20060009632A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: WPI03-0210NMIM  
; CURRENT FILING DATE: 2005-09-14  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2000-05-16  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR FILING DATE: 2001-12-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-226-701-6

Query Match 83.1%; Score 1280; DB 7; Length 320;  
Best Local Similarity 100.0%; Pred. No. 1.3e-123; Indels 0; Gaps 0;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVRAERRGSGYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFGQYFHASRLRG 87  
Db 80 GDIRLRGQTGVRAERRGSGYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFGQYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLVNVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 207  
Db 200 FKLDVMTLHRLVNVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 259

Qy 208 LAAAAHDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTIGMLRESRLLAHLPKEM 319

Qy 268 T 268  
Db 320 T 320

## RESULT 2

US-11-226-701-4  
; Sequence 4, Application US/11226701  
; Publication No. US2006009632A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; CURRENT APPLICATION NUMBER: US/11/226,701  
; CURRENT FILING DATE: 2005-09-14  
; PRIOR APPLICATION NUMBER: US/10/386,414  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: 09/426,282  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 09/668,266  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/330,970  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: 09/724,599  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/860,193  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/571,589  
; PRIOR FILING DATE: 2000-05-16  
; PRIOR APPLICATION NUMBER: 10/283,023  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/010,943  
; PRIOR FILING DATE: 2001-12-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

## US-11-226-701-4

Query Match 83.1%; Score 1280; DB 7; Length 502;  
Best Local Similarity 100.0%; Pred. No. 2.3e-123; Indels 0; Gaps 0;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVRAERRGSGYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFGQYFHASRLRG 87  
Db 80 GDIRLRGQTGVRAERRGSGYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFGQYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLVNVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 207  
Db 200 FKLDVMTLHRLVNVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMGL 259

Qy 208 LAAAAHDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTIGMLRESRLLAHLPKEM 319

Qy 268 T 268  
Db 320 T 320

## RESULT 3

US-10-492-835-8  
; Sequence 8, Application US/10492835  
; Publication No. US20050289660A2  
; GENERAL INFORMATION:  
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION  
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS  
; TITLE OF INVENTION: OF USE  
; FILE REFERENCE: MEMORY 4 WO  
; CURRENT APPLICATION NUMBER: US/10/492,835  
; CURRENT FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; LENGTH: 747  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-492-835-8

Query Match 21.5%; Score 331.5; DB 6; Length 747;  
Best Local Similarity 37.8%; Pred. No. 8.7e-26;  
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----FGQYFHASRLRGIIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121  
Db 293 KEKKRPMISQISGVKKLMHSSSLTNSCLPFGVTEQEDVDLAKE---LEDVKNKGLHVFR 349

Qy 122 FDLRLTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLVNVQEDYHSQNPYHNAVHAAD 180  
Db 350 IAEI-SGNRPLVIMHTIFQBERDLKTKPKIPVDLTILYLTMTLEDHYADVAVYNNIHAAD 408

Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLAAAAHDVDPGVNQPFLIKTNHHLANLYQNMV 240  
Db 409 VVQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSALAMYNDSS 468

Qy 241 VLENHHRSTIGMLRE 256  
Db 469 VLENHHLAVGFKLQRE 484

## RESULT 4

US-10-492-835-15  
; Sequence 15, Application US/10492835  
; Publication No. US20050289660A2  
; GENERAL INFORMATION:  
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION



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; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492.835
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-492-835-15

Query Match      21.5%, Score 331.5; DB 6; Length 747;
Best Local Similarity 37.8%; Pred. No. 8.7e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----PQRYFHASRLRLGIIPOAPLHLLDEVDYLGQARHMLSKVGMWDFDIFL 121
Db 293 KKKRPMISQGVKKMLHSSSLTNSCIPRGVKTQEDVLAKL---LEDVKNWGLHVR 349

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLFLVMQVEDYHSQNPYHNAVHAAD 180
Db 350 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTLEDDHYHADVAYHNNIHAAD 408

Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHPGVNQPLIKTNHHLANLYQMS 240
Db 409 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQPLINTNSLALMYNDSS 468

Qy 241 VLENHHRSTIGMLRE 256
Db 469 VLENHHLAVGFKLQ 484

RESULT 5
US-10-492-835-27
; Sequence 27, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492.835
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-492-835-27

Query Match      21.5%, Score 331.5; DB 6; Length 747;
Best Local Similarity 37.8%; Pred. No. 8.7e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----PQRYFHASRLRLGIIPOAPLHLLDEVDYLGQARHMLSKVGMWDFDIFL 121
Db 293 KKKRPMISQGVKKMLHSSSLTNSCIPRGVKTQEDVLAKL---LEDVKNWGLHVR 349

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLFLVMQVEDYHSQNPYHNAVHAAD 180
Db 350 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTLEDDHYHADVAYHNNIHAAD 408

Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHPGVNQPLIKTNHHLANLYQMS 240
Db 409 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQPLINTNSLALMYNDSS 468

Qy 241 VLENHHRSTIGMLRE 256
Db 469 VLENHHLAVGFKLQ 484

US-10-492-835-27

Query Match      21.5%, Score 331.5; DB 6; Length 747;
Best Local Similarity 37.8%; Pred. No. 8.7e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----PQRYFHASRLRLGIIPOAPLHLLDEVDYLGQARHMLSKVGMWDFDIFL 121
Db 293 KKKRPMISQGVKKMLHSSSLTNSCIPRGVKTQEDVLAKL---LEDVKNWGLHVR 349

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLFLVMQVEDYHSQNPYHNAVHAAD 180
Db 350 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTLEDDHYHADVAYHNNIHAAD 167

Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHPGVNQPLIKTNHHLANLYQMS 240
Db 168 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQPLINTNSLALMYNDSS 227

Qy 241 VLENHHRSTIGMLRE 256
Db 228 VLENHHLAVGFKLQ 243

US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: GretaReddottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091.018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-10

Query Match      21.5%, Score 330.5; DB 7; Length 507;
Best Local Similarity 37.8%; Pred. No. 6.6e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----PQRYFHASRLRLGIIPOAPLHLLDEVDYLGQARHMLSKVGMWDFDIFL 121
Db 52 KKKRPMISQGVKKMLHSSSLTNSCIPRGVKTQEDVLAKL---LEDVKNWGLHVR 108

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLFLVMQVEDYHSQNPYHNAVHAAD 180
Db 109 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTLEDDHYHADVAYHNNIHAAD 167

Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHPGVNQPLIKTNHHLANLYQMS 240
Db 168 VVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQPLINTNSLALMYNDSS 227

Qy 241 VLENHHRSTIGMLRE 256
Db 228 VLENHHLAVGFKLQ 243

US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: GretaReddottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091.018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
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; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-9

Query Match      21.5%; Score 330.5; DB 7; Length 585;
Best Local Similarity 37.8%; Pred. No. 8e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 130 KKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVR 186

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMVQEDYHSQNPYNNAHAAD 180
Db 187 IAEI-SGNRPLTVIMHTIFQERDLLKTKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 245

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDHPGVNQPLIKTNHHLNLYONMS 240
Db 246 VVQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQFLINTNSLALMYNDSS 305

Qy 241 VLENHHWRSTIGMLRE 256
Db 306 VLENHHLAVGFKLLQE 321

RESULT 8
US-11-091-018-6
; Sequence 6, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-6

Query Match      21.5%; Score 330.5; DB 7; Length 673;
Best Local Similarity 37.8%; Pred. No. 9.6e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;
```

```
Qy 66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 218 KKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVR 274

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMVQEDYHSQNPYNNAHAAD 180
Db 275 IAEI-SGNRPLTVIMHTIFQERDLLKTKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDHPGVNQPLIKTNHHLNLYONMS 240
Db 334 VVQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQFLINTNSLALMYNDSS 393

Qy 241 VLENHHWRSTIGMLRE 256
Db 394 VLENHHLAVGFKLLQE 409

RESULT 9
US-11-091-018-8
; Sequence 8, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-8

Query Match      21.5%; Score 330.5; DB 7; Length 687;
Best Local Similarity 37.8%; Pred. No. 9.9e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 232 KKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVR 288

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMVQEDYHSQNPYNNAHAAD 180
Db 289 IAEI-SGNRPLTVIMHTIFQERDLLKTKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 347

Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDHPGVNQPLIKTNHHLNLYONMS 240
Db 348 VVQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQFLINTNSLALMYNDSS 407

Qy 241 VLENHHWRSTIGMLRE 256
Db 408 VLENHHLAVGFKLLQE 423

RESULT 10
US-11-091-018-4
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```
; Sequence 4, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaardt, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-4

Query Match      21.5%; Score 330.5; DB 7; Length 745;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLS----FQRYFHASRLRLGIIPOAPHLHLLDEYLGQARHMLSKVGWDFDIFL 121
Db 290 KKKKRPMSQISGVKKMLHSSSLTNSIPRFGVKTQEDVLAKE---LEDVKNWGLHVR 346

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDVMTLHRLFLVMVOEDYHSQNPYHNAHAAD 180
Db 347 IAEI-SGNRPLTVIMHTIFQERDLLKTKFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 405

Qy 181 VTQAMHCYLKPKLASFLTPDLMGLLAAAHADVDPGVNQPLIKTNHHLANLYONMS 240
Db 406 VQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 465

Qy 241 VLENHHRSTIGMLRE 256
Db 466 VLENHHLAVGFKLQE 481

RESULT 11
US-10-492-835-12
; Sequence 12, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492,835
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-12

Query Match      21.5%; Score 330.5; DB 6; Length 748;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLS----FQRYFHASRLRLGIIPOAPHLHLLDEYLGQARHMLSKVGWDFDIFL 121
Db 293 KKKKRPMSQISGVKKMLHSSSLTNSIPRFGVKTQEDVLAKE---LEDVKNWGLHVR 349

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDVMTLHRLFLVMVOEDYHSQNPYHNAHAAD 180
Db 350 IAEI-SGNRPLTVIMHTIFQERDLLKTKFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy 181 VTQAMHCYLKPKLASFLTPDLMGLLAAAHADVDPGVNQPLIKTNHHLANLYONMS 240
Db 409 VQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy 241 VLENHHRSTIGMLRE 256
Db 466 VLENHHLAVGFKLQE 481

RESULT 12
US-10-492-835-28
; Sequence 28, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492,835
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-28

Query Match      21.5%; Score 330.5; DB 6; Length 748;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVKRLS----FQRYFHASRLRLGIIPOAPHLHLLDEYLGQARHMLSKVGWDFDIFL 121
Db 293 KKKKRPMSQISGVKKMLHSSSLTNSIPRFGVKTQEDVLAKE---LEDVKNWGLHVR 349

Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDVMTLHRLFLVMVOEDYHSQNPYHNAHAAD 180
Db 350 IAEI-SGNRPLTVIMHTIFQERDLLKTKFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy 181 VTQAMHCYLKPKLASFLTPDLMGLLAAAHADVDPGVNQPLIKTNHHLANLYONMS 240
Db 409 VQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy 241 VLENHHRSTIGMLRE 256
Db 466 VLENHHLAVGFKLQE 481

RESULT 13
US-11-091-018-2
; Sequence 2, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaardt, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
```



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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:00 ; Search time 166.463 Seconds  
(without alignments)  
1187.771 Million cell updates/sec

Title: US-10-781-181-5  
Perfect score: 2408  
Sequence: 1 MSCLWVRGCEILLFENPDQ.....PDHAGQGTSEBQEGDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	100.0	450	3 AAY93569	Aay93569 Amino aci
2	2408	100.0	450	4 AAU08675	Aau08675 Human pho
3	2408	100.0	450	4 AAG78915	Aag78915 Human typ
4	2401	99.7	450	8 ADP78549	Adp78549 Human pho
5	2258	93.8	502	5 ABB09005	Abb09005 Human pho
6	2258	93.8	502	8 ADJ58904	Adj58904 Human cyc
7	2234	92.8	502	4 AAB36503	Aab36503 Human lon
8	2219.5	92.2	451	3 AAY93575	Aay93575 Amino aci
9	2192	91.0	446	3 AAY93567	Aay93567 Amino aci
10	2166	90.0	446	3 AAY93574	Aay93574 Amino aci
11	2165.5	89.9	445	3 AAY93573	Aay93573 Amino aci
12	2121	88.1	437	3 AAY93572	Aay93572 Amino aci
13	1990.5	82.7	413	3 AAY93571	Aay93571 Amino aci
14	1865	77.5	391	4 AAU08676	Aau08676 Human pho
15	1801	74.8	335	9 ADY50214	Ady50214 Human PDE
16	1801	74.8	335	9 ADZ46770	Adz46770 Human PDE
17	1430	59.4	268	3 AAY93593	Aay93593 Amino aci
18	1430	59.4	288	3 AAY93568	Aay93568 Human PDE
19	1425.5	59.2	456	5 AAE24530	Aae24530 Mouse PDE
20	1419.5	58.9	482	5 AAE24531	Aae24531 Human PDE
21	1419.5	58.9	482	8 ADO40842	Ado40842 Human pho
22	1419.5	58.9	482	8 ADR46207	Adr46207 Human pho
23	1419.5	58.9	482	9 ADY18092	Ady18092 PRO poly
24	1419.5	58.9	498	2 AAU00094	Aau00094 CAMP phos

RESULT 1  
AAY93569  
XX ID AAY93569 standard; protein; 450 AA.  
XX AC AAY93569;  
XX DT 25-SEP-2000 (first entry)  
XX DE Amino acid sequence of a human phosphodiesterase enzyme.  
XX KW Phosphodiesterase; PDE-XIV; human; enzyme.  
XX OS Homo sapiens.  
XX PN EP1018559-A1.  
XX PD 12-JUL-2000.  
XX PF 09-NOV-1999; 99EP-00308902.  
XX PR 23-DEC-1998; 98GB-00028603.  
XX PR 17-SEP-1999; 99GB-00022123.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Fidoack M;  
XX WPI; 2000-433274/38.  
XX N-PSDB; AAA46651.  
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.  
XX Disclosure; Page 45-47; 104pp; English.

#### ALIGNMENTS

25 1419.5 58.9 498 2 AAY49808 Aay49808 Human gli  
26 1419.5 58.9 498 3 AAB20619 Aab20619 pTM22 hum  
27 1419.5 58.9 498 8 ADR66097 Adr66097 Human pro  
28 1419.5 58.9 498 8 ADR66439 Adr66439 Human pro  
29 1418.5 58.9 456 8 ADO21910 Ado21910 Human CAM  
30 1418.5 58.9 456 9 ADY18172 Ady18172 PRO poly  
31 1410.5 58.6 426 5 AAE24528 Aae24528 Mouse PDE  
32 1403.5 58.3 426 5 AAE24527 Aae24527 Human PDE  
33 1403.5 58.3 446 5 AAE24532 Aae24532 Human PDE  
34 1402.5 58.2 468 8 ABM83120 Abm83120 Human dia  
35 1397.5 58.0 426 5 AAE24529 Aae24529 Rat PDE7  
36 1397.5 58.0 426 5 AAE24533 Aae24533 Rat PDE7a  
37 1297 53.9 441 8 ABM83121 Abm83121 Human dia  
38 1287 53.4 424 5 AAU79727 Aau79727 Human cyc  
39 1286 53.4 432 4 AAU16967 Aau16967 Human nov  
40 1280 53.2 320 4 AAB36504 Aab36504 Human sho  
41 1280 53.2 320 8 ADJ58906 Adj58906 Human cyc  
42 1277 53.0 425 8 ABM83119 Abm83119 Human dia  
43 1261 52.4 437 8 ABM83118 Abm83118 Human dia  
44 1240.5 51.5 359 8 ADR46209 Adr46209 Human pho  
45 1239.5 51.5 354 8 ADR46211 Adr46211 Human pho

The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and

CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
 CC gene and/or expression product may be used in the preparation of a  
 CC composition for the treatment of a disorder associated with inappropriate  
 CC PDE-XIV expression and/or activity and to screen for agents that can  
 CC modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies  
 CC may also be used as diagnostic agents for detecting the presence of PDE-  
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA))  
 XX  
 XX  
 SQ Sequence 450 AA;

Query Match 100.0%; Score 2408; DB 3; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-226;  
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLWVRCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLNSTTYS 60  
 Db 1 MSCLWVRCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLNSTTYS 60  
 Qy 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGMWDFDIF 120  
 Db 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGMWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Qy 181 VTQAMHCYLKPEKPLASFLTPDLMGLLAAAHDVDPHGPNQVOPPLIKTNHHLANLYQMS 240  
 Db 181 VTQAMHCYLKPEKPLASFLTPDLMGLLAAAHDVDPHGPNQVOPPLIKTNHHLANLYQMS 240  
 Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Qy 301 KDLRLDAQDRHFMQLIALKCADICNPCRIMWMSKOWSERVCEEFYRQGELEKFELEIS 360  
 Db 301 KDLRLDAQDRHFMQLIALKCADICNPCRIMWMSKOWSERVCEEFYRQGELEKFELEIS 360  
 Qy 361 PLCNQKQDSIPSIQIGFMSYIPEPLFREWAFHTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Db 361 PLCNQKQDSIPSIQIGFMSYIPEPLFREWAFHTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Qy 421 HRSRSGSGGPDHDHAGQGTESEBEQGDSP 450  
 Db 421 HRSRSGSGGPDHDHAGQGTESEBEQGDSP 450

RESULT 2  
 AAU08675  
 ID AAU08675 standard; protein; 450 AA.  
 XX  
 AC AAU08675;

XX  
 XX 18-DEC-2001 (first entry)  
 XX  
 DE Human phosphodiesterase type 7B #1.

XX Human; phosphodiesterase type 7B; cardiovascular disease; asthma;  
 KW allergy; inflammatory disease; immune-related disorder; cardiovascular;  
 KW antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.

OS Homo sapiens.

XX WO200162940-A2.

XX 30-AUG-2001.

XX 20-FEB-2001; 2001WO-EP001858.

XX 21-FEB-2000; 2000EP-00103655.

XX

(MERE ) MERCK PATENT GMBH.

XX Kluxen F, Hentech B;

XX WFI; 2001-570636/64.

DR N-PSDB; AAS13248.

XX Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,  
 PT diagnosing and treating, e.g. asthma, inflammation and allergies.

XX Claim 1; Page 36-37; 40pp; English.

XX The invention relates to a novel human Phosphodiesterase type 7B  
 CC polypeptide and the nucleic acid that encodes it. The protein and nucleic  
 CC acid may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For  
 CC example, The protein and nucleic acid may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P7B by expressing  
 CC inactive proteins or to supplement the patients own production of P7B.  
 CC The nucleic acids may be used to produce P7B polypeptides, by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. The nucleic acid and its complements may also be used as DNA  
 CC probes in diagnostic assays to detect and quantitate the presence of  
 CC similar nucleic acids in samples, and therefore which patients may be in  
 CC need of restorative therapy. The P7B polypeptides may also be used as  
 CC antigens in the production of antibodies against P7B and in assays to  
 CC identify modulators of it's expression and activity. The anti-P7B  
 CC antibodies and antagonists may also be used to down regulate expression  
 CC and activity. The anti-P7B antibodies may also be used as diagnostic  
 CC agents for detecting the presence of P7B in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Disorders that may be prevented,  
 CC diagnosed and/or treated by the above methods include, for example  
 CC cardiovascular disease, asthma, allergy, inflammation, and immune-related  
 CC disorders. The present sequence represents a human phosphodiesterase 7B  
 XX

SQ Sequence 450 AA;

Query Match 100.0%; Score 2408; DB 4; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-226;  
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLWVRCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLNSTTYS 60  
 Db 1 MSCLWVRCGEILFENPDQNAKVCMLGDIRLQGTGVRAERGSYPFIDFRLNSTTYS 60  
 Qy 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGMWDFDIF 120  
 Db 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGMWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAAD 180  
 Qy 181 VTQAMHCYLKPEKPLASFLTPDLMGLLAAAHDVDPHGPNQVOPPLIKTNHHLANLYQMS 240  
 Db 181 VTQAMHCYLKPEKPLASFLTPDLMGLLAAAHDVDPHGPNQVOPPLIKTNHHLANLYQMS 240  
 Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Qy 301 KDLRLDAQDRHFMQLIALKCADICNPCRIMWMSKOWSERVCEEFYRQGELEKFELEIS 360  
 Db 301 KDLRLDAQDRHFMQLIALKCADICNPCRIMWMSKOWSERVCEEFYRQGELEKFELEIS 360  
 Qy 361 PLCNQKQDSIPSIQIGFMSYIPEPLFREWAFHTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Db 361 PLCNQKQDSIPSIQIGFMSYIPEPLFREWAFHTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Qy 421 HRSRSGSGGPDHDHAGQGTESEBEQGDSP 450  
 Db 421 HRSRSGSGGPDHDHAGQGTESEBEQGDSP 450

RESULT 3  
AAG78915  
ID AAG78915 standard; protein; 450 AA.  
AC AAG78915;  
XX  
XX  
DT 19-DEC-2001 (first entry)  
XX  
XX  
DE Human type 7B phosphodiesterase, PDE7B.  
XX  
XX  
KW Human; type 7B phosphodiesterase; PDE7B; enzyme.  
XX  
OS Homo sapiens.  
XX  
XX  
PN JP2001238680-A.  
XX  
XX  
PD 04-SEP-2001.  
XX  
XX  
PF 03-MAR-2000; 2000JP-00058159.  
XX  
XX  
PR 03-MAR-2000; 2000JP-00058159.  
XX  
XX  
PA (TANA ) TANABE SEIYAKU CO.  
XX  
XX  
DR WPI; 2001-610057/70.  
DR N-PSDB; AAI70009.  
XX  
XX  
PT New phosphodiesterase for use in the development of inhibitors of high  
selectivity and drugs of low side effect.  
XX  
XX  
PS Claim 2; Page 12-14; 18pp; Japanese.  
XX  
XX  
CC The present sequence is the protein sequence for human type 7B  
phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the  
development of inhibitors of high selectivity and drugs of low side  
effects  
XX  
SQ Sequence 450 AA;

Query Match 100.0%; Score 2408; DB 4; Length 450;  
Best Local Similarity 100.0%; Pred. No. 1.6e-226;  
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLWVERCGEILFENPDONAKVCMLGDIIRLQGTGVAERRSYPPIDPRLNSTTYS 60  
Db 1 MSCLWVERCGEILFENPDONAKVCMLGDIIRLQGTGVAERRSYPPIDPRLNSTTYS 60

Qy 61 GEIGTKKKVKLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120  
Db 61 GEIGTKKKVKLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120

Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180

Qy 181 VTQAMHCYLPKPKLASFLTPDIDMLGLAAAHVDHGVNQPFLLKTNHHLANLYQMS 240  
Db 181 VTQAMHCYLPKPKLASFLTPDIDMLGLAAAHVDHGVNQPFLLKTNHHLANLYQMS 240

Qy 241 VLENHWRSTIGMLRESLLAHLKEMTDIEQQLGSLILATDINRQNEFLTRLKAHLN 300  
Db 241 VLENHWRSTIGMLRESLLAHLKEMTDIEQQLGSLILATDINRQNEFLTRLKAHLN 300

Qy 301 KDLREDAQRHFMQLKALCADICNPRIWMSKQSERVCBFYRQGELEQKFELEIS 360  
Db 301 KDLREDAQRHFMQLKALCADICNPRIWMSKQSERVCBFYRQGELEQKFELEIS 360

Qy 361 PLCNQOKDSIPSIOIGFMSYIPEPLFREWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
Db 361 PLCNQOKDSIPSIOIGFMSYIPEPLFREWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420

Qy 421 HRSRSGSGPDHHDHAGCGTSESEEGDSP 450  
Db 421 HRSRSGSGPDHHDHAGCGTSESEEGDSP 450

RESULT 4  
ADP79549  
ID ADP79549 standard; protein; 450 AA.  
AC ADP79549;  
XX  
XX  
DT 04-NOV-2004 (first entry)  
XX  
XX  
DE Human phosphodiesterase 7B nucleotide sequence.  
XX  
XX  
KW Human; phosphodiesterase 7B; PDE7b; cardiovascular-gen.; CNS-Gen.;  
gynaecological; haemostatic; respiratory-Gen.; cytostatic; gene therapy;  
enzyme.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO2004044196-A1.  
XX  
XX  
PD 27-MAY-2004.  
XX  
XX  
PF 05-NOV-2003; 2003WO-EP012342.  
XX  
XX  
PR 13-NOV-2002; 2002EP-00025502.  
XX  
XX  
PA (PARB ) BAYER HEALTHCARE AG.  
XX  
XX  
PI Golz S, Brueggemeier U, Summer H;  
XX  
XX  
DR WPI; 2004-440631/41.  
DR N-PSDB; ADP79548.  
XX  
XX  
PT Screening for therapeutic agents, useful in treating cardiovascular,  
reproduction, urological, hematological, respiratory system or cancer  
diseases, comprises contacting a test compound with a phosphodiesterase  
7b.  
XX  
XX  
SQ Disclosure; SEQ ID NO 2; 128pp; English.

The present sequence is that of human phosphodiesterase 7b (PDE7b), an  
enzyme regulating intracellular levels of cAMP and cGMP. The invention  
relates to novel disease associations of PDE7b polynucleotides and  
polypeptides. It also relates to novel methods of screening for  
therapeutic agents for the treatment of cardiovascular diseases,  
disorders of the peripheral and central nervous system, reproduction  
diseases, urological diseases, haematological diseases, disorders of the  
respiratory system and cancer. PDE7b polynucleotides, polypeptides and  
regulators or modulators of PDE7b activity (e.g. an RNA molecule,  
antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used  
in the treatment or diagnosis of these diseases and disorders.

Query Match 99.7%; Score 2401; DB 8; Length 450;  
Best Local Similarity 99.8%; Pred. No. 7.6e-226;  
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSCLWVERCGEILFENPDONAKVCMLGDIIRLQGTGVAERRSYPPIDPRLNSTTYS 60  
Db 1 MSCLWVERCGEILFENPDONAKVCMLGDIIRLQGTGVAERRSYPPIDPRLNSTTYS 60

Qy 61 GEIGTKKKVKLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120  
Db 61 GEIGTKKKVKLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120

Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180



Qy 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDHDPGVNQPFLLIKTNHHLANLYQNMS 240  
 Db 181 VTQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDHDPGVNQPFLLIKTNHHLANLYQNMS 240  
 Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLIILATDINRQNEFLTRUKAHLN 300  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLIILATDINRQNEFLTRUKAHLN 300  
 Qy 301 KDLRLDAQDRHFMQLKALCADICNCRLEWMSKQMSRVCSEFYRQGELEOKFELEIS 360  
 Db 301 KDLRLDAQDRHFMQLKALCADICNCRLEWMSKQMSRVCSEFYRQGELEOKFELEIS 360  
 Qy 361 PLCNQKXDSIPSIQIGFMSYIVPELPREWAHFTGNSTLSENMLGHLAHLNKAQWKSLLPRQ 420  
 Db 361 PLCNQKXDSIPSIQIGFMSYIVPELPREWAHFTGNSTLSENMLGHLAHLNKAQWKSLLPRQ 420  
 Qy 421 HRSRSGSGDPDHDHAGQGTESEBEQGDSP 450  
 Db 421 HRSRSGSGDPDHDHAGQGTESEBEQGDSP 450  
 RESULT 5  
 ABB09005  
 ID ABB09005 standard; protein; 502 AA.  
 XX AC ABB09005;  
 XX DT 23-MAY-2002 (first entry)  
 XX DE Human phosphodiesterase-1.  
 XX KW HPDE; human phosphodiesterase; cyclic nucleotide phosphodiesterase;  
 KW antiinflammatory; neuroprotective; cytostatic; antianaemic;  
 KW immunosuppressive; HIV; cardiovascular disorder; mental disorder;  
 KW gene therapy; transgene; enzyme.  
 XX OS Homo sapiens.  
 XX PN WO2001198471-A2.  
 XX PD 27-DEC-2001.  
 XX PF 21-JUN-2001; 2001WO-US020140.  
 XX PR 22-JUN-2000; 2000US-0213741P.  
 XX PR 14-JUL-2000; 2000US-0218234P.  
 XX PR 16-OCT-2000; 2000US-0241100P.  
 XX PA (INCY-) INCYTE GENOMICS INC.  
 XX PI Thornton M, Ding L, Patterson C, Yao MG, Tribouley CM, Lal P;  
 PI Hafalia AJA, Baughn MR, Ramkumar J, Lu Y, Walia NK,  
 XX N-PSDB; ABA99136.  
 DR WPI; 2002-147799/19.  
 DR N-PSDB; ABA99136.  
 XX Novel human phosphodiesterase polypeptides and polynucleotides for  
 PT diagnosing, preventing and treating eye, neurological, cardiovascular,  
 PT cell proliferative and autoimmune/inflammatory disorders.  
 XX Claim 1; Page 97-98; 105pp; English.  
 XX This invention relates to isolated human phosphodiesterase polypeptides  
 CC (HPDE 1-4), which are antiinflammatory, neuroprotective, cytostatic,  
 CC antianaemic, immunosuppressive and anti-HIV in their action. The  
 CC polypeptides are useful for screening a compound for effectiveness as an  
 CC agonist or antagonist of the protein. The identified agonist, antagonist  
 CC and protein are useful for treating a disease or condition associated  
 CC with decreased or overexpression of functional HPDE in a patient. The  
 CC proteins are useful in preparing polyclonal or monoclonal antibodies by  
 CC hybridoma technology. They are also useful in the treatment and  
 CC prevention of eye, neurological, cardiovascular, cell proliferative and  
 CC autoimmune and inflammatory disorders, metabolic disorders and mental

CC disorders. The polynucleotides are useful for creating humanised animals  
 CC or transgenic animals to model human disease and to detect and quantify  
 CC gene expression in biopsied tissues in which expression of HPDE is  
 CC correlated with disease. HPDE, its fragments and antibodies specific for  
 CC HPDE are useful as elements on a microarray which is useful to monitor or  
 CC measure protein-protein interactions, drug-target interactions and gene  
 CC expression profiles. This sequence represents HPDE-1  
 XX SQ Sequence 502 AA;  
 Query Match 93.8%; Score 2258; DB 5; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 9e-212;  
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 28 GDRLRGQTGVRAERGSYPFDIFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87  
 Db 80 GDRLRGQTGVRAERGSYPFDIFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139  
 Qy 88 IIPQAPLHLLDELYLQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCLHFNTHGLIHH 147  
 Db 140 IIPQAPLHLLDELYLQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCLHFNTHGLIHH 199  
 Qy 148 FKLDVTLHRLVMOEDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLIMGL 207  
 Db 200 FKLDVTLHRLVMOEDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLIMGL 259  
 Qy 208 LAAAHADVDPGVNQPFLLIKTNHHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 267  
 Db 260 LAAAHADVDPGVNQPFLLIKTNHHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 319  
 Qy 268 TDIEQQLGSLIILATDINRQNEFLTRUKAHLNKAQWKSLLPRQDHDHAGQGTESEBEQ 327  
 Db 320 TDIEQQLGSLIILATDINRQNEFLTRUKAHLNKAQWKSLLPRQDHDHAGQGTESEBEQ 379  
 Qy 328 CRIWMSKQMSRVCSEFYRQGELEOKFELEISPLCNQKXDSIPSIQIGFMSYIVPELPFR 387  
 Db 380 CRIWMSKQMSRVCSEFYRQGELEOKFELEISPLCNQKXDSIPSIQIGFMSYIVPELPFR 439  
 Qy 388 EWAHFTGNSTLSENMLGHLAHLNKAQWKSLLPRQDHDHAGQGTESEBEQ 447  
 Db 440 EWAHFTGNSTLSENMLGHLAHLNKAQWKSLLPRQDHDHAGQGTESEBEQ 499  
 Qy 448 DSP 450  
 Db 500 DSP 502  
 RESULT 6  
 ADJ58904  
 ID ADJ58904 standard; protein; 502 AA.  
 XX AC ADJ58904;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human cyclic nucleotide phosphodiesterase protein #1.  
 XX KW 27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;  
 KW cellular proliferation; cellular differentiation; immune disorder;  
 KW cardiovascular disorder; endothelial cell disorder;  
 KW haematopoietic disorder; blood vessel disorder; brain disorder; pain;  
 KW metabolic disorder; liver disorder; platelet disorder; gene therapy;  
 KW human; cyclic; enzyme.  
 XX OS Homo sapiens.  
 XX PN US2004006016-A1.  
 XX PD 08-JAN-2004.  
 XX PF 11-MAR-2003; 2003US-00386414.  
 XX PR 11-JUN-1999; 99US-00330970.



PR 25-OCT-1999; 99US-00426282.  
PR 16-MAY-2000; 2000US-00571589.  
PR 22-SEP-2000; 2000US-00668266.  
PR 28-NOV-2000; 2000US-00724599.  
PR 07-DEC-2000; 2000US-0254037P.  
PR 10-APR-2001; 2001US-00833082.  
PR 16-MAY-2001; 2001US-00860193.  
PR 31-OCT-2001; 2001US-0335044P.  
PR 06-DEC-2001; 2001US-00010943.  
PR 29-OCT-2002; 2002US-00283023.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Kapeller-Libermann R, White D, Robison KE, Macbeth KJ, Carroll JM;  
PI Cook WJ, Meyers RE, Chun M, Williamson MJ;  
XX  
XX WPI; 2004-081738/08.  
DR N-PSDB; ADJ58903.  
XX  
XX New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic  
PT acid molecules, useful for diagnosing or treating cancer, pain, or  
PT immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic  
PT and liver disorders.  
XX  
XX Claim 4; SEQ ID NO 4; 245pp; English.  
XX  
XX The present invention relates to an isolated 27875, 22025, 27420, 17906,  
CC 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for  
CC diagnosing or treating cancer or aberrant cellular proliferation and/or  
CC differentiation, immune disorders, heart disorders, cardiovascular  
CC disorders including endothelial cell disorders, hematopoietic disorders,  
CC blood vessel disorders, brain disorders, pain and metabolic disorders,  
CC liver disorders and platelet disorders. The invention is also useful in  
CC gene therapy. The present sequence is human cyclic nucleotide  
CC phosphodiesterase.  
XX  
XX Sequence 502 AA;  
XX  
Query Match 93.8%; Score 2258; DB 8; Length 502;  
Best Local Similarity 100.0%; Pred. No. 9e-212;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GDIRLGGTGVRAERGSYPFIDFRLNSTTYSGEIGTKKKVRLLSFQRYFHASRLRG 87  
DB '80 GDIRLGGTGVRAERGSYPFIDFRLNSTTYSGEIGTKKKVRLLSFQRYFHASRLRG 139  
QY 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFTNTHGLIHH 147  
DB 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFTNTHGLIHH 199  
QY 148 FKLDWVTLHRLFLVMVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASFLTPDLMGL 207  
DB 200 FKLDWVTLHRLFLVMVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASFLTPDLMGL 259  
QY 208 LAAAHVDVHPGVNQPFILKTNHLLANLYQMSVLENHHRSTIGMLRESRLLAHLPKEM 267  
DB 260 LAAAHVDVHPGVNQPFILKTNHLLANLYQMSVLENHHRSTIGMLRESRLLAHLPKEM 319  
QY 268 TDIEQOGLSLIATDINRQNEFLTRKAHLNKOILEDAQDRHFMQLIATKACDINP 327  
DB 320 TDIEQOGLSLIATDINRQNEFLTRKAHLNKOILEDAQDRHFMQLIATKACDINP 379  
QY 328 CRIWEMSKQSERVCEFFYRQGELEQKFELEISPLCNQKQDSIPSIGFMSVIVBPLFR 387  
DB 380 CRIWEMSKQSERVCEFFYRQGELEQKFELEISPLCNQKQDSIPSIGFMSVIVBPLFR 439  
QY 388 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQHRSGSGSGSPGDHHDAGQGTSEBEQ 447  
DB 440 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQHRSGSGSGSPGDHHDAGQGTSEBEQ 499  
QY 448 DSP 450  
DB 500 DSP 502

RESULT 7  
AAB36503  
XX AAB36503 standard; protein; 502 AA.  
XX  
XX AAB36503;  
XX  
XX 06-MAR-2001 (first entry)  
XX  
XX Human long phosphodiesterase protein SEQ ID NO:1.  
XX  
XX Human; long phosphodiesterase; short phosphodiesterase; diagnosis;  
KW cyclic nucleotide phosphodiesterase; nootropic; cardiac; hypotensive;  
KW nephrotropic; antidepressant; antiinflammatory; immunosuppressive;  
KW antiinfertility; antiaesthetic; vasotropic; gene therapy; dementia;  
KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;  
KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;  
KW atopic disease; autoimmune encephalomyelitis; organ transplantation;  
KW nephrotic syndrome; erectile dysfunction.  
XX  
XX Homo sapiens.  
OS  
XX US6146876-A.  
PN  
XX 14-NOV-2000.  
PD  
XX 11-JUN-1999; 99US-00330970.  
XX  
XX 26-MAR-1999; 99US-00277423.  
PR  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Kapeller-Libermann R, White D, Robison KE;  
PI  
XX WPI; 2001-0233577/03.  
DR  
XX N-PSDB; AAC87948.  
DR  
XX Polynucleotide encoding novel cyclic nucleotide phosphodiesterase useful  
PT for treating disorders related with to protein e.g. dementia,  
PT hypertension, glomerulonephritis, and organ transplantation.  
XX  
XX Claim 3; Fig 1; 42pp; English.  
PS  
XX The present sequence represents the human long phosphodiesterase which is  
CC a cyclic nucleotide phosphodiesterase (I). (I) can have nootropic,  
CC cardiac, hypotensive, nephrotropic, antidepressant, antiinflammatory,  
CC immunosuppressive, antiinfertility, antiaesthetic and vasotropic  
CC activities, and can be used in gene therapy. (II) can be used for treating  
CC various disorders associated or mediated by (I), such as dementia,  
CC amnesia, congestive heart failure, thrombosis, pulmonary hypertension,  
CC glomerulonephritis, bipolar depression, bronchial asthma, atopic  
CC diseases, autoimmune encephalomyelitis, organ transplantation, salt  
CC retention in nephrotic syndrome and erectile dysfunction  
XX  
XX Sequence 502 AA;  
XX  
Query Match 92.8%; Score 2234; DB 4; Length 502;  
Best Local Similarity 99.1%; Pred. No. 2e-209;  
Matches 419; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 28 GDIRLGGTGVRAERGSYPFIDFRLNSTTYSGEIGTKKKVRLLSFQRYFHASRLRG 87  
DB 80 GDIRLGGTGVRAERGSYPFIDFRLNSTTYSGEIGTKKKVRLLSFQRYFHASRLRG 139  
QY '88 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFTNTHGLIHH 147  
DB 140 IIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFTNTHGLIHH 199  
QY 148 FKLDWVTLHRLFLVMVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASFLTPDLMGL 207  
DB 200 FKLDWVTLHRLFLVMVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASFLTPDLMGL 259

Qy 208 LAAAHVDVHGVPQFLIKTNHHLANLYQNMSVLENHHWRSTTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAHVDVHGVPQFLIKTNHHLGALYQNMSVLENHHWRSTTIGMLRESRLLAHLPKEM 319  
Qy 268 TDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNP 327  
Db 320 TDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNP 379  
Qy 328 CRIWEMSKQSERVCEFYRGELEQKFELEISPLCNCQKDSIPSIQIGMSYIVPELFR 387  
Db 380 CRIWEMSKQSERVCEFYRGELEQKFELEISPLCNCQKDSIPSIQIGMSYIVPELFR 439  
Qy 388 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPQHRHRSRSGSGDPDHDHAGOGTSEBQEG 447  
Db 440 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPQHRHRSRSGSGDPDHDHAGOGTSEBQEG 499  
Qy 448 DSP 450  
Db 500 DSP 502  
  
RESULT 8  
AA93575  
ID AA93575 standard; protein; 451 AA.  
XX  
AC AA93575;  
XX  
DT 25-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of a phosphodiesterase enzyme.  
XX  
KW Phosphodiesterase; PDE-XIV; enzyme.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 12  
FT /label= Val, Ile  
FT Misc-difference 16  
FT /label= Ser, Asn  
FT Misc-difference 18  
FT /label= Glu, Asp  
FT Misc-difference 20  
FT /label= Ser, Val, Asn, Ala  
FT Misc-difference 21  
FT /label= Ser, Val, Asn, Ala  
FT Misc-difference 30  
FT /label= Val, Ile  
FT Misc-difference 39  
FT /label= Pro, Arg  
FT Misc-difference 56  
FT /label= Asn, Ser  
FT Misc-difference 59  
FT /label= His, Tyr  
FT Misc-difference 114  
FT /label= Thr, Met  
FT Misc-difference 141  
FT /label= Ser, Thr  
FT Misc-difference 168  
FT /label= Gly, His, Ser, Gln  
FT Misc-difference 169  
FT /label= Gly, His, Ser, Gln  
FT Misc-difference 307  
FT /label= Asp, Ala, Asn, Val  
FT Misc-difference 308  
FT /label= Asp, Ala, Asn, Val  
FT Misc-difference 350  
FT /label= Glu, Asp  
FT Misc-difference 379  
FT /label= Ser, Thr  
FT Misc-difference 391  
FT /label= His, Arg  
FT Misc-difference 404

FT Misc-difference /label= Gly, Ser  
FT 418  
FT Misc-difference /label= Pro, Arg, Ser, Asn  
FT 419  
FT Misc-difference /label= Pro, Arg, Ser, Asn  
FT 423  
FT Misc-difference /label= Ser, Arg  
FT 435  
FT Misc-difference /label= His, Leu  
FT 439..440  
FT /note= "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"  
FT Misc-difference 442..443  
FT /note= "these residues are either Ser-Glu or Thr-Leu"  
FT Misc-difference 446  
FT /note= "optionally absent"  
FT Misc-difference 449..450  
FT /note= "these residues are either Asp-Ser or Ala-Thr"  
XX  
PN EP1018559-A1.  
XX  
PD 12-JUL-2000.  
XX  
PF 09-NOV-1999; 99EP-00308902.  
XX  
PR 23-DEC-1998; 98GB-00028603.  
PR 17-SEP-1999; 99GB-00022123.  
XX  
PA (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX  
PI Fidock M;  
XX  
DR WPI; 2000-433274/38.  
XX  
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.  
PT  
PS Disclosure; Page 75-78; 104pp; English.  
XX  
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))  
XX  
SQ Sequence 451 AA;

Query Match 92.2%; Score 2219.5; DB 3; Length 451;  
Best Local Similarity 93.1%; Pred. No. 4.6e-208;  
Matches 420; Conservative 0; Mismatches 30; Indels 1; Gaps 1;  
  
Qy 1 MSCLMVRCGEITLFPENPDONAKVCVCMGLDIRLGRGQTVGAERGSYPFFIDFRLNNTYS 60  
Db 1 MSCLMVRCGEITLFPENPDONAKVCVCMGLDIRLGRGQTVGAERGSYPFFIDFRLNNTYS 60  
Qy 61 GEIGTKKKVKRLLSFQRYFHASRLRGIIPQAPLHLLDELYLQOARHMLSKVGMWDFDIF 120

Db 61 GEIGTKKKVRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
 Qy 181 VTOAMHCYLPKPKLASFPLTDIMGLLAAAHVDHHPGVNQPFLIKTNHHLNLYQNS 240  
 Db 181 VTOAMHCYLPKPKLASFPLTDIMGLLAAAHVDHHPGVNQPFLIKTNHHLNLYQNS 240  
 Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Qy 301 KDLRLDAQDRHFLMQIALKCADICNPCIWEMSKQMSERVCBEFYRQGELEQKFELEIS 360  
 Db 301 KDLRLDAQDRHFLMQIALKCADICNPCIWEMSKQMSERVCBEFYRQGELEQKFELEIS 360  
 Qy 361 PLCNQKQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Db 361 PLCNQKQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Qy 421 HRSRSGSGGPDHHDHAGQGTSEEQ-EGDSP 450  
 Db 421 HRSRSGSGGPDHHDHAGQGTSEEQ-EGDSP 451

## RESULT 9

AAY93567  
 ID AAY93567 standard; protein; 446 AA.  
 AC AAY93567;

XX 25-SEP-2000 (first entry)  
 XX Amino acid sequence of a murine phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; murine; enzyme.

XX Mus sp.

XX EPI018559-A1.

XX 12-JUL-2000.

XX 09-NOV-1999; 99EP-00308902.

XX 23-DEC-1998; 98GB-00028603.

PR 17-SEP-1999; 99GB-00022123.

XX (PFIZ ) PFIZER LTD.

PA (PFIZ ) PFIZER INC.

FI Fidock M;

XX WPI; 2000-433274/38.

DR N-PSDB; AAA46649.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
 PT useful for preventing diagnosing and treating diseases associated with  
 FT inappropriate PDE-XIV expression and/or activity.

XX Disclosure; Page 39-41; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
 CC phosphodiesterase polynucleotide and polypeptide may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
 CC administered to treat diseases by rectifying mutations or deletions in a  
 CC patient's genome that affect the activity of PDE-XIV. They may also be  
 CC used to study the expression and function of PDE-XIV polypeptides and  
 CC their role in metabolism. The PDE-XIV polypeptides may be used as

CC antigens in the production of antibodies against PDE-XIV and in assays to  
 CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
 CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
 CC gene and/or expression product may be used in the preparation of a  
 CC composition for the treatment of a disorder associated with inappropriate  
 CC PDE-XIV expression and/or activity and to screen for agents that can  
 CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
 CC may also be used as diagnostic agents for detecting the presence of PDE-  
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA))  
 XX  
 SQ Sequence 446 AA;

Query Match 91.0%; Score 2192; DB 3; Length 446;

Best Local Similarity 91.6%; Pred. No. 2.2e-205;

Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

Qy 1 MSCLMVERCCEIILFENPDQNAKVCVCMGLDRLRGOTGVRAERRGSYPFIDPRLNLTYS 60  
 Db 1 MSCLMVERCCEIILFENPDQNAKVCVCMGLDRLRGOTGVRAERRGSYPFIDPRLNLTYS 60  
 Qy 61 GEIGTKKKVRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120  
 Db 61 GEIGTKKKVRLLSFQRYFHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDFDIF 120  
 Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
 Qy 181 VTOAMHCYLPKPKLASFPLTDIMGLLAAAHVDHHPGVNQPFLIKTNHHLNLYQNS 240  
 Db 181 VTOAMHCYLPKPKLASFPLTDIMGLLAAAHVDHHPGVNQPFLIKTNHHLNLYQNS 240  
 Qy 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Db 241 VLENHWRSTIGMLRESRLLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRKKAHLN 300  
 Qy 301 KDLRLDAQDRHFLMQIALKCADICNPCIWEMSKQMSERVCBEFYRQGELEQKFELEIS 360  
 Db 301 KDLRLDAQDRHFLMQIALKCADICNPCIWEMSKQMSERVCBEFYRQGELEQKFELEIS 360  
 Qy 361 PLCNQKQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Db 361 PLCNQKQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420  
 Qy 421 HRSRSGSGGPDHHDHAGQGTSEEQ-EGDSP 450  
 Db 421 HRSRSGSGGPDHHDHAGQGTSEEQ-EGDSP 446

## RESULT 10

AAY93574  
 ID AAY93574 standard; protein; 446 AA.

AC AAY93574;

XX 25-SEP-2000 (first entry)

XX Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

XX Synthetic.

XX Key... Location/Qualifiers  
 FT Misc-difference 12 /label= Val, Ile  
 FT Misc-difference 16 /label= Ser, Asn  
 FT Misc-difference 18 /label= Glu, Asp  
 FT Misc-difference 20

FT /label= Ser, Val, Asn, Ala  
 FT Misc-difference 21  
 FT /label= Ser, Val, Asn, Ala  
 FT Misc-difference 30  
 FT /label= Val, Ile  
 FT Misc-difference 39  
 FT /label= Pro, Arg  
 FT Misc-difference 56  
 FT /label= Asn, Ser  
 FT Misc-difference 59  
 FT /label= His, Tyr  
 FT Misc-difference 114  
 FT /label= Thr, Met  
 FT Misc-difference 141  
 FT /label= Ser, Thr  
 FT Misc-difference 168  
 FT /label= Gly, His, Ser, Gln  
 FT Misc-difference 169  
 FT /label= Gly, His, Ser, Gln  
 FT Misc-difference 307  
 FT /label= Asp, Ala, Asn, Val  
 FT Misc-difference 308  
 FT /label= Asp, Ala, Asn, Val  
 FT Misc-difference 350  
 FT /label= Glu, Asp  
 FT Misc-difference 379  
 FT /label= Ser, Thr  
 FT Misc-difference 391  
 FT /label= His, Arg  
 FT Misc-difference 404  
 FT /label= Gly, Ser  
 FT Misc-difference 418  
 FT /label= Pro, Arg, Ser, Asn  
 FT Misc-difference 419  
 FT /label= Pro, Arg, Ser, Asn  
 FT Misc-difference 423  
 FT /label= Ser, Arg  
 FT Misc-difference 430  
 FT /label= His, Leu  
 FT Misc-difference 433  
 FT /label= Gln, Gly, Thr, Pro, Ala  
 FT Misc-difference 434  
 FT /label= Gln, Gly, Thr, Pro, Ala  
 FT Misc-difference 435  
 FT /label= Gln, Gly, Thr, Pro, Ala  
 FT Misc-difference 437  
 FT /label= Ser, Glu, Thr, Leu  
 FT Misc-difference 438  
 FT /label= Ser, Glu, Thr, Leu  
 FT Misc-difference 441  
 FT /note= "optionally absent"  
 FT Misc-difference 444  
 FT /label= Asp, Ser, Ala, Thr  
 FT Misc-difference 445  
 FT /label= Asp, Ser, Ala, Thr  
 XX EP1018559-A1.  
 XX 12-JUL-2000.  
 XX 09-NOV-1999; 99EP-00308902.  
 XX 23-DEC-1998; 98GB-00028603.  
 XX 17-SEP-1999; 99GB-00022123.  
 XX (PF12 ) PFIZER LTD.  
 XX (PF12 ) PFIZER INC.  
 XX Fidoack M;  
 XX WPI; 2000-433274/38.  
 XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,

PT useful for preventing diagnosing and treating diseases associated with  
 PT inappropriate PDE-XIV expression and/or activity.  
 XX Disclosure; Page 70-72; 104pp; English.  
 XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
 CC enzyme sequence is derived from a formula of the invention. The  
 CC phosphodiesterase polynucleotide and polypeptide may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
 CC administered to treat diseases by rectifying mutations or deletions in a  
 CC patient's genome that affect the activity of PDE-XIV. They may also be  
 CC used to study the expression and function of PDE-XIV polypeptides and  
 CC their role in metabolism. The PDE-XIV polypeptides may be used as  
 CC antigens in the production of antibodies against PDE-XIV and in assays to  
 CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
 CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
 CC gene and/or expression product may be used in the preparation of a  
 CC composition for the treatment of a disorder associated with inappropriate  
 CC PDE-XIV expression and/or activity and to screen for agents that can  
 CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
 CC may also be used as diagnostic agents for detecting the presence of PDE-  
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA)).  
 XX SQ Sequence 446 AA;  
 Query Match 90.0%; Score 2166; DB 3; Length 446;  
 Best Local Similarity 91.6%; Pred. No. 7,8e-203;  
 Matches 413; Conservative 0; Mismatches 32; Indels 6; Gaps 2;  
 QY 1 MSCLMVRCGEILFENPDONAKVCVCMGLDIRLGRGTVGAERGSYPFIDFRLNNTYS 60  
 DB 1 MSCLMVRCGEXLFXEPXQXXKVCVCMGLGDXRLRGTVGAERGSYPFIDFRLNNTXS 60  
 QY 61 GEIGTKKKVKRLLSFORYFHASRLRLGIIPOAPLHLLDEDEDYLGQARHMLS KVGWDFDIF 120  
 DB 61 GEIGTKKKVKRLLSFORYFHASRLRLGIIPOAPLHLLDEDEDYLGQARHMLS KVGWDFDIF 120  
 QY 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
 DB 121 LFDRLTNGNSLVTLCHLNFTHGLIHHFKLDVMVTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
 QY 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDVHPGVNQPFLIKTNHHLANLYQNMS 240  
 DB 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDVHPGVNQPFLIKTNHHLANLYQNMS 240  
 QY 241 VLENHHWRSTIGMLRESRLLAHLPKEMTODIEQQLGSLILATDINRQNEFLTRKALHN 300  
 DB 241 VLENHHWRSTIGMLRESRLLAHLPKEMTODIEQQLGSLILATDINRQNEFLTRKALHN 300  
 QY 301 KDLRLDAQDRHFMQLQALKCADICNPCRIMWSKQWSERVCEEFYRQGELEOKFELEIS 360  
 DB 301 KDLRLLEXQDRHFMQLQALKCADICNPCRIMWSKQWSERVCEEFYRQGELEOKFELEIS 360  
 QY 361 PLCNQOKOSIPSIQIGFMSYIYVEPLPREWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
 DB 361 PLCNQOKOSIPSIQIGFMSYIYVEPLPREWAXFTGNSTLSENMLGHLAHNAQWKSLLXXQ 420  
 QY 421 HRSRSGSGGPDHDHAGQCTESEEQ-EGDSP 450  
 DB 421 HXRSGS-----QDXAGXXKXKXETEGXXP 446  
 RESULT 11  
 ID AAY93573  
 XX AAY93573 standard; protein; 445 AA.  
 AC AAY93573;  
 XX 25-SEP-2000 (first entry)  
 XX

DE XX Amino acid sequence of a phosphodiesterase enzyme.  
KW XX Phosphodiesterase; PDE-XIV; enzyme.  
OS XX Synthetic.  
XX XX  
XX XX Key Location/Qualifiers  
PH FT Misc-difference 12 /label= Val, Ile  
FT FT Misc-difference 16 /label= Ser, Asn  
FT FT Misc-difference 18 /label= Glu, Asp  
FT FT Misc-difference 20..21 /label= Ser, Val, Asn, Ala  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 30 /label= Val, Ile  
FT FT Misc-difference 39 /label= Pro, Arg  
FT FT Misc-difference 56 /label= Asn, Ser  
FT FT Misc-difference 59 /label= His, Tyr  
FT FT Misc-difference 114 /label= Thr, Met  
FT FT Misc-difference 141 /label= Ser, Thr  
FT FT Misc-difference 168..169 /label= Gly, His, Ser, Gln  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 307..308 /label= Asp, Ala, Asn, Val  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 350 /label= Glu, Asp  
FT FT Misc-difference 379 /label= Ser, Thr  
FT FT Misc-difference 391 /label= His, Arg  
FT FT Misc-difference 404 /label= Gly, Ser  
FT FT Misc-difference 418..419 /label= Pro, Arg, Ser, Asn  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 423 /label= Ser, Arg  
FT FT Misc-difference 423 /label= Ser, Arg  
FT FT Misc-difference 427..428 /label= Ser, Gly, Pro, Asp, His, Gln  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 430 /label= His, Leu  
FT FT Misc-difference 433..434 /label= Gln, Gly, Thr, Pro, Ala  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 436..437 /label= Ser, Glu, Thr, Leu  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
FT FT Misc-difference 440 /note= "optionally absent"  
FT FT Misc-difference 443..444 /label= Asp, Ser, Ala, Thr  
FT FT /note= "these residues are a peptide comprising at least  
FT FT two or more of the above residues"  
XX XX

PN EPI018559-A1.  
XX 12-JUL-2000.  
PD XX  
XX 09-NOV-1999; 99EP-00308902.  
XX 23-DEC-1998; 98GB-00028603.  
XX 17-SEP-1999; 99GB-00022123.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Fido M;  
XX WPI; 2000-433274/38.  
DR XX  
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
FT useful for preventing diagnosing and treating diseases associated with  
FT inappropriate PDE-XIV expression and/or activity.  
XX  
XX Disclosure; Page 64-66; 104pp; English.  
XX  
XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC enzyme sequence is derived from a formula of the invention. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
CC administered to treat diseases by rectifying mutations or deletions in a  
CC patient's genome that affect the activity of PDE-XIV. They may also be  
CC used to study the expression and function of PDE-XIV polypeptides and  
CC their role in metabolism. The PDE-XIV polypeptides may be used as  
CC antigens in the production of antibodies against PDE-XIV and in assays to  
CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
CC gene and/or expression product may be used in the preparation of a  
CC competition for the treatment of a disorder associated with inappropriate  
CC PDE-XIV expression and/or activity and to screen for agents that can  
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
CC may also be used as diagnostic agents for detecting the presence of PDE-  
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
CC (ELISA))  
XX  
SQ Sequence 445 AA;  
Query Match 89.9%; Score 2165.5; DB 3; Length 445;  
Best Local Similarity 91.3%; Pred. No. 8.7e-203;  
Matches 411; Conservative 1; Mismatches 33; Indels 5; Gaps 1;  
Qy 1 MSCIMVERCGEILFENPDQNAKVCVCMGLDTRLRGQTGVRAERGRGSPFIDPRLINSTYS 60  
Db 1 MSCIMVERCGEXLFXPXQXXKVCVCMGLDGLXRLRGQTGVAXAERGRGSPFIDPRLINXTYS 60  
Qy 61 GEIGTKKKVKRLISFQRYPHASRLRGIIIPQAPLHLLDEYLGQARHMLSKVGWMDIF 120  
Db 61 GEIGTKKKVKRLISFQRYPHASRLRGIIIPQAPLHLLDEYLGQARHMLSKVGWMDIF 120  
Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWTLHRLFLVMVQEDYHSQNPYHNAHAAD 180  
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDWTLHRLFLVMVQEDYHXXNPYHNAHAAD 180  
Qy 181 VTQAMCHYLKEPKLASPLTPDLMGLLAAAHDVDPGVNQPPILKTNHHLANLYQNS 240  
Db 181 VTQAMCHYLKEPKLASPLTPDLMGLLAAAHDVDPGVNQPPILKTNHHLANLYQNS 240  
Qy 241 VLENHHRSTIGMLRSRLAHPKEMTDIEQOLGSLIATDINRQNEFLTRKAHLN 300  
Db 241 VLENHHRSTIGMLRSRLAHPKEMTDIEQOLGSLIATDINRQNEFLTRKAHLN 300  
Qy 301 KDLRLDAQDRHFMLOIALKACADICNPCRISWMSKQWSEVCEFFYRQGELEQKFELEIS 360  
Db 301 KDLRLDAQDRHFMLOIALKACADICNPCRISWMSKQWSEVCEFFYRQGELEQKFELEIS 360

Qy 361 PLCNQKDSIPSIQIGFMYSIVIEPLFREWAFHTGNTSLSENMLGHLAHNAQWKSLPRQ 420  
Db 361 PLCNQKDSIPSIQIGFMYSIVIEPLFREWAFHTGNTSLSENMLGHLAHNAQWKSLPRQ 420  
Qy 421 HRSRGSSGSPDHPDHACQGTSEHQEGDSP 450  
Db 421 HXRGRSX-----XDXAGXEXXEQTEGXXP 445

## RESULT 12

AA933572  
ID AA933572 standard; protein; 437 AA.

XX AC AAY933572;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of a phosphodiesterase enzyme.

XX KW Phosphodiesterase; PDE-XIV; enzyme.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 12 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 16 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 18 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 20 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 29 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 38 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 55 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 58 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 113 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 140 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 167 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 305 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 347 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 376 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 388 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 401 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 415 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 419 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 423 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 425 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 428 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 430 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 433 /note= "any suitable peptide sequence or amino acid"  
FT Misc-difference 436 /note= "any suitable peptide sequence or amino acid"  
XX /note= "any suitable peptide sequence or amino acid"

PN EP1018559-A1.  
XX 12-JUL-2000.  
XX 09-NOV-1999; 99EP-00308902.  
XX 23-DEC-1998; 98GB-00028603.  
PR 17-SEP-1999; 99GB-00022123.  
XX (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX Fidoack M;  
XX WPI; 2000-433274/38.  
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
FT useful for preventing diagnosing and treating diseases associated with  
FT inappropriate PDE-XIV expression and/or activity.  
XX Disclosure; Page 58-60; 104pp; English.  
XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC enzyme sequence is derived from a formula of the invention. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
CC administered to treat diseases by rectifying mutations or deletions in a  
CC patient's genome that affect the activity of PDE-XIV. They may also be  
CC used to study the expression and function of PDE-XIV polypeptides and  
CC their role in metabolism. The PDE-XIV polypeptides may be used as  
CC antigens in the production of antibodies against PDE-XIV and in assays to  
CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
CC gene and/or expression product may be used in the preparation of a  
CC composition for the treatment of a disorder associated with inappropriate  
CC PDE-XIV expression and/or activity and to screen for agents that can  
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
CC may also be used as diagnostic agents for detecting the presence of PDE-  
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
XX (ELISA))  
SQ Sequence 437 AA;

Query Match 88.1%; Score 2121; DB 3; Length 437;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-198;  
Matches 411; Conservative 1; Mismatches 23; Indels 12; Gaps 6;  
QY 1 MSCLMVERGCEILFENPDQNAKCVCMGDIRLIRGOTGVRAERRGSYPFFIDFRLNNTTYS 60  
Db 1 MSCLMVERGCEILFENPDQNAKCVCMGDIRLIRGOTGVRAERRGSYPFFIDFRLNNTTYS 59  
QY 61 GIGTKKKVKRLLSFQRYPHASRLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIF 120  
Db 60 GIGTKKKVKRLLSFQRYPHASRLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIF 119  
QY 121 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMVQEDYHSONPVHNAHAAD 180  
Db 120 LFDRLTNGNSLVTLCHLNFTHGLIHFFKLDVMTLHRLFLVMVQEDYHSONPVHNAHAAD 178  
QY 181 VTQAMHCYKPEKPLASFLTPDLMGLLAAAADVDHVGWNPQFPLKTNHHLANLQNMMS 240  
Db 179 VTQAMHCYKPEKPLASFLTPDLMGLLAAAADVDHVGWNPQFPLKTNHHLANLQNMMS 238  
QY 241 VLENHHRSTIGWLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN 300  
Db 239 VLENHHRSTIGWLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN 298  
QY 301 KDLRLDAQDRHFMLOIALKCADICNPCRIMWMSKQWSEVCEEFYRQGELEKQKFELEIS 360  
Db 299 KDLRLDAQDRHFMLOIALKCADICNPCRIMWMSKQWSEVCEEFYRQGELEKQKFELEIS 357

QY 361 PLCNQKDSIPSIQIGFMSYIVPLFREWAFHTGNTSLSENMLGHLAHNAQWKSLLPRQ 420  
|||  
DB 358 PLCNQKDSIPSIQIGFMSYIVPLFREWAFHTGNTSLSENMLGHLAHNAQWKSLL-XQ 416  
|||  
QY 421 HRSRSGSGPDHDHAGQGQTESREQ 447  
|||  
DB 417 HRXRGSK-----DXA--GXEXEQEG 435  
|||

## RESULT 13

AAU93571  
ID AAY93571 standard; protein; 413 AA.  
XX  
AC AAY93571;  
XX  
DT 25-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

XX Synthetic.

XX EPI018559-A1.

PD 12-JUL-2000.

XX 09-NOV-1999; 99EP-00308902.

XX 23-DEC-1998; 98GB-00028603.

PR 17-SEP-1999; 99GB-00022123.

XX (PFIZ ) PFIZER LTD.

PA (PFIZ ) PFIZER INC.

XX Fidoack M;

XX WFI; 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
PT useful for preventing diagnosing and treating diseases associated with  
PT inappropriate PDE-XIV expression and/or activity.

XX Claim 2; Page 55-57; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC enzyme sequence is derived from a formula of the invention. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide be  
CC administered to treat diseases by rectifying mutations or deletions in a  
CC patient's genome that affect the activity of PDE-XIV. They may also be  
CC used to study the expression and function of PDE-XIV polypeptides and  
CC their role in metabolism. The PDE-XIV polypeptides may be used as  
CC antigens in the production of antibodies against PDE-XIV and in assays to  
CC identify modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be  
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV  
CC gene and/or expression product may be used in the preparation of a  
CC composition for the treatment of a disorder associated with inappropriate  
CC PDE-XIV expression and/or activity and to screen for agents that can  
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies  
CC may also be used as diagnostic agents for detecting the presence of PDE-  
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
CC (ELISA))

XX Sequence 413 AA;

XX Query Match 82.7%; Score 1990.5; DB 3; Length 413;  
XX Best Local Similarity 90.8%; Pred. No. 1.1e-185;  
XX Matches 406; Conservative 1; Mismatches 5; Indels 35; Gaps 16;

QY 1 MSCLMVERCCEILFENPDQNAKVCMLGDIRLGRQTGVRARRGSGYPFIDFRLNLTYS 60

DB 1 MSCLMVERCCE-LFE-----PQKCVMLGD-RLRGQTV-AERRGSPFIDFRLNLT--S 51  
|||  
QY 61 GEIGTKKKVKRLLSFQRYPHASRLRGIIPOAPLHLLDEYLGQARHMLSKVGWDPDIF 120  
|||  
DB 52 GEIGTKKKVKRLLSFQRYPHASRLRGIIPOAPLHLLDEYLGQARHMLSKVG-WDPDIF 110  
|||  
QY 121 LFDRLTNGSLVTLTLLCHLNFTHGLIHHFKLDVMTLHRLVVMQEDYHSONPYHNAVHAAD 180  
|||  
DB 111 LFDRLTNGSLVTLTLLCHLNF-HGLIHHFKLDVMTLHRLVVMQEDYH--NPYHNAVHAAD 167  
|||  
QY 181 VTQAMHCYLKEPKLASFLTPLDIMLGILAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMS 240  
|||  
DB 168 VTQAMHCYLKEPKLASFLTPLDIMLGILAAAHDVDHPGVNQPFLLIKTNHHLANLYQNMS 227  
|||  
QY 241 VLENHHRSTIGMLRESRLLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRIKAHLHN 300  
|||  
DB 228 VLENHHRSTIGMLRESRLLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRIKAHLHN 287  
|||  
QY 301 KDLRLDAQDRHEMLQIALKCADICNPCRITWMSKOWSERVCEEFYRQGLEOKFELEIS 360  
|||  
DB 288 KDLRLD--QDRHEMLQIALKCADICNPCRITWMSKOWSERVCEEFYRQGLEOKFELEIS 344  
|||  
QY 361 PLCNQKDSIPSIQIGFMSYIVPLFREWAFHTGNTSLSENMLGHLAHNAQWKSLLPRQ 420  
|||  
DB 345 PLCNQKDSIPSIQIGFM-YIVEPLFREWAFHTGNTSLSENML-HLAHNAQWKSLL--Q 399  
|||  
QY 421 HRSRSGSGPDHDHAGQGQTESREQ 447  
|||  
DB 400 HR-RGSDA-----GEEQEG 412  
|||

RESULT 14  
AAU08676  
ID AAU08676 standard; protein; 391 AA.  
XX  
AC AAU08676;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human phosphodiesterase type 7B #2.  
XX  
KW Human; phosphodiesterase type 7B; cardiovascular disease; asthma;  
KW allergy; inflammatory disease; immune-related disorder; cardiovascular;  
KW antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT Misc-difference 188 /label= Unknown  
FT /note= "Encoded by CMC"  
FT Misc-difference 188 /note= "Encoded by GAR"  
FT Misc-difference 387 /label= Unknown  
FT /note= "Encoded by GNN"  
XX  
PN WC200162940-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-EP001858.  
XX  
PR 21-FEB-2000; 2000EP-00103655.  
XX  
PA (MERE ) MERCK PATENT GMBH.  
XX  
PI Kluxen F., Hentsch B;  
XX  
DR WPI; 2001-570636/64.  
DR N-PSDB; AAS13249.  
XX



PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,  
PT diagnosing and treating, e.g. asthma, inflammation and allergies.  
PS Claim 1; Page 39-40; 4Opp; English.  
XX  
CC The invention relates to a novel human Phosphodiesterase type 7B  
CC polypeptide and the nucleic acid that encodes it. The protein and nucleic  
CC acid may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For  
CC example, The protein and nucleic acid may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of P7B by expressing  
CC inactive proteins or to supplement the patients own production of P7B.  
CC The nucleic acids may be used to produce P7B polypeptides, by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. The nucleic acid and its complements may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar nucleic acids in samples, and therefore which patients may be in  
CC need of restorative therapy. The P7B polypeptides may also be used as  
CC antigens in the production of antibodies against P7B and in assays to  
CC identify modulators of it's expression and activity. The anti-P7B  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-P7B antibodies may also be used as diagnostic  
CC agents for detecting the presence of P7B in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA)). Disorders that may be prevented,  
CC diagnosed and/or treated by the above methods include, for example  
CC cardiovascular disease, asthma, allergy, inflammation, and immune-related  
CC disorders. The present sequence represents a human phosphodiesterase 7B  
XX Sequence 391 AA;

Query Match 77.5%; Score 1865; DB 4; Length 391;  
Best Local Similarity 92.7%; Pred. No. 2e-173;  
Matches 354; Conservative 2; Mismatches 26; Indels 0; Gaps 0;  
QY 52 RLNNSTTSGEIGTKKKVRLLSFQRYFHASRLRGIIPQAPHLHLDDEYLGQARHMLSK 111  
DB 10 RLNNSTTSGEIGTKKKVRLLSFQRYFHASRLRGIIPQAPHLHLDDEYLGQARHMLSK 69  
QY 112 VGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRFLVNVQEDYHSQNP 171  
DB 70 VGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRFLVNVQEDYHSQNP 129  
QY 172 YHNAVHAADVTQAMHCYKPKLASFLTPDIDMLGLLAAAHDVDHPGVNQPELIKTNIH 231  
DB 130 YHNAVHAADVTQAMHCYKPKLASFLTPDIDMLGLLAAAHDVDHPGVNQPELIKTNIH 189  
QY 232 LANLYQNMVLENHHRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLIATDINRQNEFL 291  
DB 190 LANLYQNMVLENHHRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLIATDINRQNEFL 249  
QY 292 TRLKAHLHNKDLRLDAQDRHFMLOALKCADICNCRWEMSKQNSRVCSEFYRQGE 351  
DB 250 TRLKAHLHNKDLRLDAQDRHFMLOALKCADICNCRWEMSKQNSRVCSEFYRQGE 309  
QY 352 EQKFELEISPLCNQKQDSIPSIQIFWMSYIVPELPFEWAHFTGNSLTSENMLGHLAHNKA 411  
DB 310 EQKFELEISPLCNQKQDSIPSIQIFWMSYIVPELPFEWAHFTGNSLTSENMLGHLAHNKA 369  
QY 412 QWKSLLPQHRSGSGSGSDPH 433  
DB 370 QWKSLLPSPSTEAGAAAXGLDH 391

RESULT 15  
ADY50214  
ID ADY50214 standard; protein; 335 AA.

XX  
AC ADY50214;  
XX  
DT 19-MAY-2005 (first entry)  
XX  
DE Human PDE7B phosphodiesterase domain SEQ ID NO:23.

XX phosphodiesterase 7B; PDE5A; X-ray crystallography; enzyme.  
XX Homo sapiens.  
XX US2005048573-A1.  
XX 03-MAR-2005.  
XX 03-FEB-2004; 2004US-00771833.  
XX 03-FEB-2003; 2003US-0444734P.  
XX 07-JUL-2003; 2003US-0485627P.  
XX (PLEX-) PLEXIKON INC.  
XX Artis DR, Bollag G, Card G, Martin F, Milburn MV, Zhang K;  
XX WPI; 2005-202088/21.  
XX Development of ligands binding to phosphodiesterase-5A (PDE5A) comprises  
XX identifying PDE5A binding compounds, determining orientation of molecular  
XX scaffold, identifying chemical structures of molecular scaffolds and  
XX synthesizing ligand.  
XX Disclosure; SEQ ID NO 23; 111pp; English.  
XX The invention relates to a novel method for development of ligands  
XX binding to phosphodiesterase-5A (PDE5A). The method comprises identifying  
XX one or more compounds as molecular scaffolds that bind to a binding site  
XX of PDE5A, determining the orientation of at least one molecular scaffold  
XX in co-crystals with PDE5A, identifying chemical structures of the  
XX molecular scaffolds, and synthesizing a ligand with altered binding  
XX affinity and/or binding specificity. The method to identify the potential  
XX PDE5A binding compounds comprises either removing a computer  
XX representation of a compound complexed with PDE5A or modifying a computer  
XX addition of one or more chemical groups; fitting a computer  
XX representation of a compound from a computer database with a computer  
XX representation of the active site of PDE5A; and identifying compounds  
XX derived from the molecular scaffold that best fit the active site based  
XX on favorable geometric fit and energetically favorable complementary  
XX interactions as potential binding compounds; and further comprises  
XX searching a database for compounds having structural similarity to the  
XX molecular scaffold or derivative compound using a compound searching  
XX computer program or replacing portions of the compound with similar  
XX chemical structures using a compound construction computer program. The  
XX compound complexed with PDE5A is non-hydrolyzable cyclic guanosine  
XX monophosphate (cGMP) analog. The fitting comprises determining whether  
XX the compounds will interact with one or more of conserved PDE5A active  
XX site residues. The attachment component is a linker (a traceless linker)  
XX for attachment to a solid phase medium and comprises a label comprising a  
XX fluorophore. The attachment method further comprises attaching the  
XX compound or derivative to a solid phase medium through a linker attached  
XX at the energetically allowed site. The phosphodiesterase comprises  
XX conserved residues matching at least one conserved PDE5A active site  
XX residues. The phosphodiesterase binding compound or derivative is  
XX synthesized on the linker attached to the solid phase medium. The  
XX plurality of the compounds or derivatives is synthesized in combinatorial  
XX synthesis. The attachment of the compounds to the solid phase medium  
XX provides an affinity medium. The present sequence represents the  
XX phosphodiesterase domain of human phosphodiesterase 7B.  
XX Sequence 335 AA;

Query Match 74.8%; Score 1801; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2.9e-167;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 GIIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLHFNTHGLI 146  
DB 1 GIIPQAPHLHLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLHFNTHGLI 60



Qy 147 HFKLDWVTLHREFLVMVOEDYHSQNPYHNVAHADVTQAMHCYLKEPKLASFLTPLDIMLG 206  
Db 61 HFKLDWVTLHREFLVMVOEDYHSQNPYHNVAHADVTQAMHCYLKEPKLASFLTPLDIMLG 120  
Qy 207 LLA AAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLIAHLPK 266  
Db 121 LLA AAAHDVDHPGVNQPFLLKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLIAHLPK 180  
Qy 267 MTODIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLBDAQDRHPMLOIALKCADICN 326  
Db 181 MTODIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLBDAQDRHPMLOIALKCADICN 240  
Qy 327 PCRIWENSKOMSERVCBEFYRQGELEKFELEISPLCNQOKDSIPSIQIGFMSYIVEPLF 386  
Db 241 PCRIWENSKOMSERVCBEFYRQGELEKFELEISPLCNQOKDSIPSIQIGFMSYIVEPLF 300  
Qy 387 REWAHFTGNSTLSENMLGHLAHNAQWKSLLPROH 421  
Db 301 REWAHFTGNSTLSENMLGHLAHNAQWKSLLPROH 335

Search completed: March 10, 2006, 19:56:52  
Job time : 167.463 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:57:15 ; Search time 31.0976 Seconds  
(without alignments)  
1392.313 Million cell updates/sec

Title: US-10-781-181-5  
Perfect score: 2408  
Sequence: 1 MSCLMVERGCEILFENPDQN.....PDHAGQGTSEBQEGDSP 450  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	100.0	450	JC7266	3',5'-cyclic-nucle
2	1419.5	58.9	498	A47286	3',5'-cyclic-AMP p
3	604.5	25.1	673	B13158	3',5'-cyclic-nucle
4	603.5	25.1	584	B53109	3',5'-cyclic-nucle
5	603.5	25.1	672	I61259	3',5'-cyclic-nucle
6	580.5	24.1	562	I59143	CAMP phosphodiesterase
7	580.5	24.1	564	A40949	cyclic-AMP phospho.
8	567.5	23.6	564	JC1519	3',5'-cyclic-nucle
9	567.5	23.6	736	I61354	phosphodiesterase
10	565	23.5	886	A54442	3',5'-cyclic-nucle
11	559.5	23.2	610	I67946	3',5'-cyclic-nucle
12	559.5	23.2	844	I53865	phosphodiesterase
13	553	23.0	712	S71626	3',5'-cyclic-nucle
14	529.5	22.0	536	I67945	3',5'-cyclic-nucle
15	517	21.5	549	T16769	hypothetical prote
16	493	20.5	777	S65543	3',5'-cyclic-nucle
17	477.5	19.8	323	S55348	3',5'-cyclic-nucle
18	468	19.4	267	B33904	CAMP phosphodiesterase
19	468	19.4	535	A46378	3',5'-cyclic-nucle
20	467	19.4	534	A44162	3',5'-cyclic-nucle
21	466	19.4	519	T14783	hypothetical prote
22	466	19.4	535	A44161	3',5'-cyclic-nucle
23	461	19.1	664	T24459	hypothetical prote
24	454.5	18.9	530	A45334	3',5'-cyclic-nucle
25	452.5	18.8	768	T10796	3',5'-cyclic-nucle
26	449	18.6	536	JC6129	3',5'-cyclic-nucle
27	445.5	18.5	713	JW0088	3',5'-cyclic-nucle
28	441	18.3	659	JB0293	3',5'-cyclic-nucle
29	441	18.3	885	JC7898	3',5'-cyclic-nucle

30	409	17.0	491	2	A40283	3',5'-cyclic-nucle
31	381	15.8	875	1	JW0106	3',5'-cyclic-GMP p
32	377	15.7	875	1	A48719	3',5'-cyclic-GMP p
33	370	15.4	1054	2	T30901	cyclic nucleotide
34	368.5	15.3	1112	2	S70522	cyclic nucleotide
35	357.5	14.8	1108	2	A48508	cyclic-nucleotide
36	346	14.4	1141	2	A44093	CGMP-inhibited CAM
37	302.5	12.6	858	2	JC4520	3',5'-cyclic-GMP p
38	300	12.5	855	2	A34810	3',5'-cyclic-GMP p
39	299	12.4	928	1	JC2486	3',5'-cyclic-nucle
40	296	12.3	921	1	A40981	3',5'-cyclic-nucle
41	283	11.8	853	2	A36617	3',5'-cyclic-GMP p
42	279	11.6	856	1	A47451	3',5'-cyclic-GMP p
43	278	11.5	856	2	S30762	3',5'-cyclic-GMP p
44	277.5	11.5	854	2	A42828	3',5'-cyclic-GMP p
45	269.5	11.2	862	2	I50186	3',5'-cyclic-GMP p

ALIGNMENTS

RESULT 1

JC7266  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human  
N/Alternate names: CAMP-specific phosphodiesterase 7B  
C/Species: Homo sapiens (man)  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: JC7266  
R/Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.  
Biochem. Biophys. Res. Commun. 271, 575-583, 2000  
A/Title: Identification of human PDE7B, a CAMP-specific phosphodiesterase.  
A/Reference number: JC7266  
A/Accession: JC7266  
A/Molecule type: mRNA  
A/Residues: 1-450 <SAS>  
A/Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040  
A/Experimental source: caudate nucleus  
C/Genetics:  
A/Gene: pde7B  
A/Map position: 6q23-24  
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C/Keywords: phosphoric diester hydrolase

Query Match	100.0%	Score	2408	DB	2	Length	450
Best Local Similarity	100.0%	Pred. No.	5.4e-182				
Matches	450	Conservative	0	Mismatches	0	Indels	0
QY	1	MSCLMVERGCEILFENPDQNAKVCVCMGLDIRLGOTGVRAERGSYPFFIDFRLINSTYS	60				
DB	1	MSCLMVERGCEILFENPDQNAKVCVCMGLDIRLGOTGVRAERGSYPFFIDFRLINSTYS	60				
QY	61	GEIGTKKKVKRLLSFORYPHARSLRLLGIIPQAPLHLLDDYLGQARHMLSKVGMWDFDIF	120				
DB	61	GEIGTKKKVKRLLSFORYPHARSLRLLGIIPQAPLHLLDDYLGQARHMLSKVGMWDFDIF	120				
QY	121	LFDRLTNGNSLVTLCHLFNTHGLIHFFKLDVMTLHRLFLVMVQEDYHSQNPYHNAVHAAD	180				
DB	121	LFDRLTNGNSLVTLCHLFNTHGLIHFFKLDVMTLHRLFLVMVQEDYHSQNPYHNAVHAAD	180				
QY	181	VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHVGPNQFPFLIKTNHHLANLQNMS	240				
DB	181	VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHVGPNQFPFLIKTNHHLANLQNMS	240				
QY	241	VLENHHRSTIGWLRESRLLAHLPKEMTODIEQQLGSLILATDINRQNEFLTKLKAHLHN	300				
DB	241	VLENHHRSTIGWLRESRLLAHLPKEMTODIEQQLGSLILATDINRQNEFLTKLKAHLHN	300				
QY	301	KDLRLLEDAQDRHFMLQIALKCAIDINPCRIWMSKQWSERVCEEYRQGELEKFELEIS	360				
DB	301	KDLRLLEDAQDRHFMLQIALKCAIDINPCRIWMSKQWSERVCEEYRQGELEKFELEIS	360				
QY	361	PLCNQOKSDIPSIOIGFMSYIIEPLFREWAHTGTSTLSENMLGHLAHNAKQWKSLLPRQ	420				

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Db      361 PLCNQKDSIPSIQGFMSYIVELFREWHAFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
Qy      421 HRSRGSGSPDHDHAGQGTESEBEGDSP 450
        |||||
Db      421 HRSRGSGSPDHDHAGQGTESEBEGDSP 450
        |||||

RESULT 2
A47286
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000
C:Accession: A47286
R:Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers, J. Biol. Chem. 268, 12925-12932, 1993
A>Title: Isolation and characterization of a previously undetected human cAMP phosphodiesterase 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-phosphoric diester hydrolase
A:Reference number: A47286; MUID:93286141; PMID:8399765
A:Accession: A47286
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-498 <MTC>
A:Cross-references: UNIPARC:UPI00001440E6; GB:L12052; NID:g1798932; PID:g179893
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-phosphoric diester hydrolase
C:Keywords: phosphoryl nucleotides
F:227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>

Query Match          58.9%; Score 1419.5; DB 2; Length 498;
Best Local Similarity 61.7%; Pred. No. 5e-104;
Matches 263; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

Qy      7 ERCEILFENPDQNAKCVMGLDIRLGQTGVRAERGSYPPIDFRLLNSTTYSGBIGTK 66
       :||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||
Db     62 QRRGAISYSSDOTALVIRMGDVVRVSRAGESERRGSHPYIDFRIFHSQSIEIUSVA 121
       ::::::::::::::::::::|||::||::||::||::||::||::||::||::||::||::||

Qy     67 KKVKRIISFORYPHASRLRGIIPQAPLHLLDDYLGOARHMLSKEGMWDFFDLFDRLT 126
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    122 RNIIRLLSFORYLRSSRPFGRTAVSNLSNLTDYYNQAKCMLEKVGNNWFIDFLFDRLT 181
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy    127 NGNSLVTLCLFNTHGLIHHEKLDMVTILHRFLVMVQEDYHSONPVHNAAADTVQAHH 186
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   182 NGNSLVSLTHLFSLHGLIIFYHLDWMKRFLVQLQEDYHSONPVHNAAADTVQAHH 241
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy   187 CYLKPKIASFLTPLDIMLGLLAAAAADVDPHGVPQPFLLIKTNHHLANLYQNMSVLNFHH 246
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   242 CYLKPKIANSVTPMDILLSLIAATHLDHPGVQPPELLIKTNHYLATLVKNTSVLENHH 301
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy   247 WRSTIGHRESRLLAHLPEMTODIQEQGLSILLATDINRFNEFLTRKAHLNKDLRLR 306
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   302 WRSAGVLLRESGLFSHLPLESROQMETQIGALITLATDISRONLEYLSLFRSHLDGRGLCLE 361
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy   307 DAQRHFMLQIALKCADI CNPCRIWMSKWSECVCEEFYRGELOSKFELETSLPNCNQ 366
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   362 DTRRHVLVLMALKACDI CNPCTWELSKWSKVTEEFFHQGDIEKKYHLGVSPLCDDR 421
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy   367 KDPSIPTQIGFMSYIVEPLFREWAHTGNSTLSENMLGHLAHNKAQWKSLLPRQRSRGS 426
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   422 TESIANIQGFMYLVEPLETFEWARTS-NTRLTSOTWLGHVGLNKASKWGLOREQSSDET 480
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy     427 SGS 429
       ;
Db     481 DAA 483

RESULT 3
161358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, CAMP-specific - human
N:Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C:Accession: I61358; I36416
R:Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993
A>Title: A family of human phosphodiesterases homologous to the duncle learning and memory

```

A:Reference number: A54442; MUID:94019330; PMID:8413254  
A:Accession: I61358  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-673 <RES>  
A:Cross-references: UNIPARC:UPI0000050EB5; GB:I20970; NID:9347129; PIDN:AAA03592.1; PID:9  
R:Baeker, P.A.; Oernolte, R.; Bach, C.; Yee, C.; Shelton, E.R.  
Gene 138, 253-256, 1994  
A:Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiesterase  
A:Reference number: I38416; MUID:94171048; PMID:8125310  
A:Accession: I38416  
A:Molecule type: mRNA  
A:Residues: 70-507, 'P', 509-673 <RES>  
A:Cross-references: UNIPARC:UPI000016A067; EMBL:U02882; NID:9433346; PIDN:AAAC13745.1; PII  
C:Genetics:  
A:Gene: GDB:PDB4D; DPDE3  
A:Cross-references: GDB:I32541; OMIM:600129  
A:Map position: 5q12-5q12  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent, 3',5'  
C:Keywords: cAMP binding; phosphoric diester hydrolase  
F:325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 25.1%; Score 604.5; DB 2; Length 673;  
Best Local Similarity 33.3%; Pred. No. 1.3e-39;  
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVKRLLS----PQRYFHASRLRGIIPOAPLHLLDDYLGOARHMLSKVGMWDFDIFL 121  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 122 FDLRTNGSLVTLTLC--LFNTHGLIHFFKLDVMTLHRLFMVQEDYHSQNPYHNAVHAAD 180  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 275 IAEI-SGNRPITVIMHTIFQERDLLKFKIPVDLTITVLTLEOHYHADVAYHNNIHAAD 333  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 181 VTQAMHCYLKEPKLASFLPTDLMGLLAAAHVDHPGVNQPFLLKTNHHLANLYQNMS 240  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 334 VVQSTHLLSTPALEAVFTLEILAAIFASAIHDVHPGVSNQFLINTNSELALMYNDSS 393  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 241 VLENHWRSTIGMLRES--LLAHLPKMTODIEQQLGSLILATDINRQNEFLTRKAHL 298  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 394 VLENHLLAVGFKLQENCDIFQNLTKQROSLRQVIVLADTMSKHMNLLADLKTNV 453  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 299 HNKO-----LRLEADAQRHFMQLIALKCADICNPCIWMSKQSERVCEFFYRQGELE 352  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 454 ETKKVTSSGVLLDNYSDRIQVLQNVHVCADLSNPTKPLQYRWQTDRIEMEEFFRQGDRE 513  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 353 QKFELEISPLCNQOKDIPSIIQIGMSYIVPEPLPREVAHFTGNSTLSENMLGHLAHNAQ 412  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 514 RERGMEISPMCDKHNASVEKSSQGVFDIYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 413 WKSLLPQHRSRSSGSGPDHDHAGGTSE-----BOEGDS 449  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
Qy 572 YQSTIPO-----SPSPAPDDPEEGQGQTEKFOFELTLEEDGES 610  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||

RESULT 4  
B53109  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form 2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: B53109; A34414; C33904; I67944  
R:Monaco, L.; Vicini, E.; Conti, M.  
J. Biol. Chem. 269, 347-357, 1994  
A:Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p  
A:Reference number: A53109; MUID:94103234; PMID:8276818  
A:Accession: B53109  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-584 <MON>  
A:Cross-references: UNIPROT:P14270; UNIPARC:UPI000002A6E1; GB:U01280  
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989  
A:Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormones

A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-672 <RES>  
A;Cross-references: UNIPARC:UPI00001759B7; EMBL:U09457; NID:G517418; PID:G517419  
A;Accession: A53678  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 167-672 <RES>  
A;Cross-references: UNIPARC:UPI00001707C8; EMBL:U09456; NID:G517416; PIDN:AAA20393.1; PII  
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.  
Gene 149, 237-244, 1994  
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes  
A;Reference number: 153865; MUID:95047482; PMID:7958996  
A;Accession: 167943  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 'N', 96-625, 'Y', 627-672 <RES>  
A;Cross-references: UNIPARC:UPI0000170BF4; GB:L27059; NID:G436007; PIDN:AAA56857.1; PID:G  
C;Genetics:  
A;Gene: PDB3/IVd gene  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C;Keywords: CAMP binding; phosphoric diester hydrolase  
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 25.1%; Score 603.5; DB 2; Length 672;  
Best Local Similarity 33.3%; Pred. No. 1.5e-39;  
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

Qy 66 KKKVKRLLS---FORYFHASRLRGRIPOAPLHLLDDEYLGQARHMLSKVGMWDFDIFL 121  
Db 218 KKKGRPMISQISGVKLMHSSSLTNSCIIPRGVTEQEDVLAK---LEDVKNKGLHVF 274  
Qy 122 FDLRTNGSLVTLTCH-LFNTHGLIHHFKLDVMTLHREFLVMVQEDYHSONPYHNAVHAAD 180  
Db 275 IAEI-SCNRPLTVIMHTIFQERDLKTKPIVDTLITVLTMTLEDHYHADVAYHNNIHAAD 333  
Qy 181 VTQAMHCYLKEPKLASFLTPDIDIMGLIAAAHVDDHGVNQPPFLIKTNHHHLANLYQNMS 240  
Db 334 VQOSTHYLLSTPALAEAVFTDLEILAAIPASAIHDVDPGVSNQFLINTNSELALMYNDSS 393  
Qy 241 VLENHHWRSITIGMLRESR--LLAHLPKEMTODIEQQLGSLILATDINRQNEFLTRLKAHL 298  
Db 394 VLENHHLAVGFKLQENECDFQNLTKKQSRKMAIDVILATDMSKRNLLADLKTWV 453  
Qy 299 HNKD-----LRLEDAQORHMLQIALKCADICNPRCWMSKOWSERVCEBFYRQGELE 352  
Db 454 ETKKVTSVGVLNDYSDRIQVLQNVHVCADLSNPKLPQLYRQWTDRIWEEFFRGQDRE 513  
Qy 353 QKFELETSPICNQKQDSIPSTQIGFMSYIVPLPFEWAHFTGNSTLSENMLGHLAHNKAQ 412  
Db 514 RERGMEISPMCKDNASVEKSVQGVFDYIVHPLWETWADLVHPD--AQDILTLEDNREW 571  
Qy 413 WKSLLPQHRSRGSSGGSPDHAGQGTSE-----EQBGDS 449  
Db 572 YQSTIPQ-----SPSPAPDQEDRGQGTKEKFQFELTLEEDGES 610

RESULT 6  
I59143  
CAMP phosphodiesterase - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I59143  
R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989  
A;Title: Isolation and characterization of a mammalian gene encoding a high-affinity CAMI  
A;Reference number: I59143; MUID:89264471; PMID:2542941  
A;Accession: I59143  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-562 <RES>  
A;Cross-references: UNIPROT:P14646; UNIPARC:UPI00001440E1; GB:J04563; NID:G203967; PIDN:G  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-

F;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 562;  
Best Local Similarity 31.9%; Pred. No. 7.7e-38;  
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;  
A:Accession: I67942  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-564 <RES>  
A:Cross-references: UNIPARC:UPI000002A6D9; GB:I27058; NID:g950096; PIDN:AAA74478.1; PID:9  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C:Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase  
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

QY 66 KKKVKKLLS-----FQRYFHASRLRLLGIIIPAQLHLDELDYLGOARHMLSKVGMWDFDIFL 121  
DB 124 KKKKQQLMTQISGVKKLMHSSSLNNTSISRGVNTENEDHLAKELEDLNK---WGLNIEN 180  
QY 122 FDLRTNGNSLVTLCHLNFTHGLIHFHFKLDWVTLHRLFLVMQVDYHSQNPYNVAHAADV 181  
DB 181 VAGYSHNRPLTTCIMYAIQFQERDLTKFKISSDTFTVYMTLEDHYHSDVAYHNSLHAADV 240  
QY 182 TQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDVHPGVNQPLIKTNHHLANLYQMNSV 241  
DB 241 AQSTHVLSTPALDAVFTDLEILAAIFAAAIHVDVHPGVNSQFLINTNSSELALMYNDESV 300  
QY 242 LENHHRSTIGMLRESR--LLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRLKAHLH 299  
DB 301 LENHHLAVGFKLLQEBHCDIFQNLTKKQRTLRKQVIMVLAATDMSKMSLLADLKTWYE 360  
QY 300 NKD-----LRLEDAQDRHFMQLKADICNPICRIWMSKQWSEVCEEFYRQGELEQ 353  
DB 361 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLLEYRQWTDRIIMEEFQOQDKER 420  
QY 354 KFELEISPLCNQOKSDIPSIOIGFMSYIVPEPLFRWAHFTGNSTSENMLGHLAHNAQW 413  
DB 421 ERGMELSPMCDKHTASVEKSGVGFIDYIVHPLWETWADLVQPD--AQDILTDLTDNRNRY 478  
QY 414 KSLPR-----QHRSGSSGSGPDH-----AGQGTSEEEQGDSP 450  
DB 479 QSMIPQSPPLDERSRDCQGLMEKQFELTLEEDSEGEKEGEGP 525

RESULT 7  
A40949  
cyclic-AMP phosphodiesterase (EC 3.1.4.-) - rat  
N:Alternate names: PDE4/IVb long form  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 09-Jul-2004  
C:Accession: A40949; D33904; A53109; I67942  
R:Swinnen, J.V.; Teikalas, K.E.; Conti, M.  
J. Biol. Chem. 266, 18370-18377, 1991  
A:Title: Properties and hormonal regulation of two structurally related cAMP phosphodies  
A:Reference number: A40949; MUID:92011578; PMID:1655746  
A:Accession: A40949  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-564 <SWI>  
A:Cross-references: UNIPROT:P14646; UNIPARC:UPI000002A6D9; GB:M25350  
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989  
A:Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP P  
A:Reference number: A33904; MUID:89315790; PMID:2546153  
A:Accession: D33904  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 210-476 <SW2>  
A:Cross-references: UNIPARC:UPI00001759B3; GB:M25350  
R:Monaco, L.; Vicini, E.; Conti, M.  
J. Biol. Chem. 269, 347-357, 1994  
A:Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP P  
A:Reference number: A53109; MUID:94103234; PMID:8276818  
A:Accession: A53109  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358, 'S', 360-564 <MON>  
A:Cross-references: UNIPARC:UPI0000170820; GB:U01291; NID:g409826; PIDN:AAAL8926.1; PID:  
R:Boiger, G.B.; Rodgers, L.K.; Riggs, M.  
Gene 149, 237-244, 1994  
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes  
A:Reference number: I53865; MUID:95047482; PMID:7958996

A:Accession: I67942  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-564 <RES>  
A:Cross-references: UNIPARC:UPI000002A6D9; GB:I27058; NID:g950096; PIDN:AAA74478.1; PID:9  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C:Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase  
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 564;  
Best Local Similarity 31.9%; Pred. No. 7.7e-38;  
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;  
A:Accession: I67942  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-564 <RES>  
A:Cross-references: UNIPARC:UPI000002A6D9; GB:I27058; NID:g950096; PIDN:AAA74478.1; PID:9  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C:Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase  
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

QY 66 KKKVKKLLS-----FQRYFHASRLRLLGIIIPAQLHLDELDYLGOARHMLSKVGMWDFDIFL 121  
DB 126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRGVNTENEDHLAKELEDLNK---WGLNIEN 182  
QY 122 FDLRTNGNSLVTLCHLNFTHGLIHFHFKLDWVTLHRLFLVMQVDYHSQNPYNVAHAADV 181  
DB 183 VAGYSHNRPLTTCIMYAIQFQERDLTKFKISSDTFTVYMTLEDHYHSDVAYHNSLHAADV 242  
QY 182 TQAMHCYLKEPKLASFLTPDLIMGLLAAAHVDVHPGVNQPLIKTNHHLANLYQMNSV 241  
DB 243 AQSTHVLSTPALDAVFTDLEILAAIFAAAIHVDVHPGVNSQFLINTNSSELALMYNDESV 302  
QY 242 LENHHRSTIGMLRESR--LLAHLPKEMTDIEQQLGSLILATDINRQNEFLTRLKAHLH 299  
DB 303 LENHHLAVGFKLLQEBHCDIFQNLTKKQRTLRKQVIMVLAATDMSKMSLLADLKTWYE 362  
QY 300 NKD-----LRLEDAQDRHFMQLKADICNPICRIWMSKQWSEVCEEFYRQGELEQ 353  
DB 363 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLLEYRQWTDRIIMEEFQOQDKER 422  
QY 354 KFELEISPLCNQOKSDIPSIOIGFMSYIVPEPLFRWAHFTGNSTSENMLGHLAHNAQW 413  
DB 423 ERGMELSPMCDKHTASVEKSGVGFIDYIVHPLWETWADLVQPD--AQDILTDLTDNRNRY 480  
QY 414 KSLPR-----QHRSGSSGSGPDH-----AGQGTSEEEQGDSP 450  
DB 481 QSMIPQSPPLDERSRDCQGLMEKQFELTLEEDSEGEKEGEGP 527

## RESULT 8

JC1519  
3',5'-cyclic-nucleotide phosphodiesterase (man)  
C:Species: Homo sapiens (man)  
C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: JC1519; A45500; I61359  
R:Obornolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, K.  
Gene 129, 239-247, 1993  
A:Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a n  
A:Reference number: JC1519; MUID:93314968; PMID:8392015  
A:Accession: JC1519  
A:Molecule type: mRNA  
A:Residues: 1-564 <OBE>  
A:Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014CSAB; GB:I12686  
A:Experimental source: lymphocyte  
A:Note: only partial nucleotide sequence is given  
R:McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.  
J. Biol. Chem. 268, 6470-6476, 1993  
A:Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.  
f mRNA  
A:Reference number: A45500; MUID:93203241; PMID:8384210  
A:Accession: A45500  
A:Molecule type: mRNA  
A:Residues: 1-564 <MCL>  
A:Cross-references: UNIPARC:UPI000014CSAB; GB:M97515; NID:g292387; PIDN:AAA36426.1; PID:9  
A:Experimental source: frontal cortex  
A:Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBI:127930)  
R:Boiger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A:Title: A family of human phosphodiesterases homologous to the dunce learning and memory  
A:Reference number: A54442; MUID:94019330; PMID:8413254

A:Accession: I61359  
A:Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-564 <RES>  
A:Cross-references: UNIPARC:UPI000014CSAB; GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
C:Keywords: phosphoric diester hydrolase  
F:233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 564;  
Best Local Similarity 31.3%; Pred. No. 8.1e-37;  
Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

QY 66 KKKVKLLS-----FQRYFHASRLRGIIIPQAPHLHDEYLGQAREHLSKVGWDFDIFL 121  
DB 126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKBEDLNK---WGLNIFN 182  
QY 122 FDLRTNGNSLVTLCHLNFTHGTHLHFKLDVMTLHFLVNVQDYHSQNPYHNAHAADV 181  
DB 183 VAGYSHNRPLTCIMYALFQERDLKTKFRISSTDTFYMTLTEDHYSDVAYNSLHAADV 242  
QY 182 TQAMHCYLKEPKLASFLTPDIDIMGLLAAAHDVDHPGVNQPELTKTNHHLNLYQNMVS 241  
DB 243 AQSTHLLSTPALDAVFTDLEILAAIFAAAHVDHDPGVSNQFLINTNSLALMYNDES 302  
QY 242 LENHWRSTIGMLRES--LLAHLPEMTQDIEQQGLSLILATDINRQNEFLTRLKAHLH 299  
DB 303 LENHHLAVGFKLQAEHCDFWNLTQKQRTLRKQVDMVLATDMSKHSLADLKTWVE 362  
QY 300 NKD-----LRLEDAQDRHFMQLKACADICNPRIWEMSKOWSERVCEEFYRQGELEQ 353  
DB 363 TKKVTSSGVLNLDNYTDRIQVLRNMVHCADLSNPTKSLDYRQWTDRIEMEEFQQQDKER 422  
QY 354 KFELEISPLCNQKQDIPSIQIGFMSYIPEPLREWAHFTGNTSLSENMLGHLAHNAQW 413  
DB 423 ERGMEISPCDKHTASVEKSVQGFIDYIVHPLWETWADLVQPD--AQDILTLEDNRNMY 480  
QY 414 KSLPLQHRSGSSGGP-----DHDHAG-----QGTSEEEQEGD 448  
DB 481 QSMIPQ-----SPSPPLDEQNRDQGLMEKFQFELTDEEDSEGEKEGE 525

RESULT 9  
I61354  
phosphodiesterase - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I61354  
R:Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A:Title: A family of human phosphodiesterases homologous to the dunce learning and memoi  
A:Reference number: A54442; MUID:94019330; PMID:8413254  
A:Accession: I61354  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-736 <RES>  
A:Cross-references: UNIPROT:Q07343; UNIPARC:UPI0000127BF6; GB:L20966; NID:g347121; PIDN:  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-  
F:405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 736;  
Best Local Similarity 31.3%; Pred. No. 1.2e-36;  
Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

QY 66 KKKVKLLS-----FQRYFHASRLRGIIIPQAPHLHDEYLGQAREHLSKVGWDFDIFL 121  
DB 298 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKBEDLNK---WGLNIFN 354  
QY 122 FDLRTNGNSLVTLCHLNFTHGTHLHFKLDVMTLHFLVNVQDYHSQNPYHNAHAADV 181  
DB 355 VAGYSHNRPLTCIMYALFQERDLKTKFRISSTDTFYMTLTEDHYSDVAYNSLHAADV 414  
QY 182 TQAMHCYLKEPKLASFLTPDIDIMGLLAAAHDVDHPGVNQPELTKTNHHLNLYQNMVS 241

DB 415 AQSTHLLSTPALDAVFTDLEILAAIFAAAHVDHDPGVSNQFLINTNSLALMYNDES 474  
QY 242 LENHWRSTIGMLRES--LLAHLPEMTQDIEQQGLSLILATDINRQNEFLTRLKAHLH 299  
DB 475 LENHHLAVGFKLQAEHCDFWNLTQKQRTLRKQVDMVLATDMSKHSLADLKTWVE 534  
QY 300 NKD-----LRLEDAQDRHFMQLKACADICNPRIWEMSKOWSERVCEEFYRQGELEQ 353  
DB 535 TKKVTSSGVLNLDNYTDRIQVLRNMVHCADLSNPTKSLDYRQWTDRIEMEEFQQQDKER 594  
QY 354 KFELEISPLCNQKQDIPSIQIGFMSYIPEPLREWAHFTGNTSLSENMLGHLAHNAQW 413  
DB 595 ERGMEISPCDKHTASVEKSVQGFIDYIVHPLWETWADLVQPD--AQDILTLEDNRNMY 652  
QY 414 KSLPLQHRSGSSGGP-----DHDHAG-----QGTSEEEQEGD 448  
DB 653 QSMIPQ-----SPSPPLDEQNRDQGLMEKFQFELTDEEDSEGEKEGE 697

RESULT 10  
A54442  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, CAMP-specific, long splice f  
N:Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form  
C:Species: Homo sapiens (man)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: A54442; S55788; A36317; S55787  
R:Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A:Title: A family of human phosphodiesterases homologous to the dunce learning and memoi  
A:Reference number: A54442; MUID:94019330; PMID:8413254  
A:Accession: A54442  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-886 <RES>  
A:Cross-references: UNIPROT:P27815; UNIPARC:UPI0000047003; GB:L20965; NID:g347119; PIDN:  
R:Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.  
Cell. Signal. 6, 793-812, 1994  
A:Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a h  
A:Reference number: S55788; MUID:95194817; PMID:7888306  
A:Accession: S55788  
A:Molecule type: mRNA  
A:Residues: 'MCPFPVTV', 210-735 'E', 737-886 <SUL>  
A:Cross-references: UNIPARC:UPI000002A6CE; EMBL:U18087; NID:g604374; PIDN:AAC50458.1; PI  
R:Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Davi  
Mol. Cell. Biol. 10, 2678-2686, 1990  
A:Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic A  
A:Reference number: A36317; MUID:90258854; PMID:2160582  
A:Accession: A36317  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 'MCPFPVTV', 210-516 'Y', 518-722 'R', 724-726 'R', 728-735 'E', 737-788 'E', 790-  
A:Cross-references: UNIPARC:UPI000017C062; GB:M37744  
C:Genetics:  
A:Gene: GDB:PDE4A; DPDE2  
A:Cross-references: GDB:138776; OMIM:600126  
A:Map position: 19p13.1-19q12  
C:Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase  
F:432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.5%; Score 565; DB 2; Length 886;  
Best Local Similarity 32.1%; Pred. No. 2.4e-36;  
Matches 126; Conservative 82; Mismatches 165; Indels 20; Gaps 6;

QY 69 VKELLSFQRYFHASRLRGIIIPQAPHLHDEYLGQAREHLSKVGWDFDIFLDTLNG 128  
DB 332 MSQITGLKMLHNSLNNSNIPFRGVTKTQDELLAQELELNK---WGLNIFCVSYAG 398  
QY 129 NSLVTLLCHLNFTHGLIHHFKLDVMTLHFLVNVQDYHSQNPYHNAHAADVQAMHCY 188  
DB 389 RSLTCIMYMIQERDLKTKFRIPVDTMTYMTLTEDHYHADVAYNSLHAADVLSQTHVL 448

Qy	189	LKEPKLASFLTPDLDMGLGLAAAHVDVHGVGNQVFPFLIKTNHHLANLYQNMVLENHHR	248
Db	449	LATPALDAVFDTLEILAAALFAAAIHDVHGVSNQFLINTNSELAMYNDESULENHHLA	508
Qy	249	STIGMLRESR--LLAHLPKEMWTODIEOQLGSLILLATDINRQNEFLTLKAHLNKKD----	302
Db	509	VGFKLLEDNCDFQNLKSKQRQSLRKWIDMVLATDMSKHMTLADLKTMTVETKVTSS	568
Qy	303	--LRLDAQDRHFMLQIALKADICNPCRISWMSKQSERVCEFYRQGLEQKFELEIS	360
Db	569	GVLLLDNYSDRIQVLRNVHVCADLSNTKPLELYRQWTDRIAMAEFFQGGDRERGRMEIS	628
Qy	361	PLCNQKQDSIPSIQIGPMYSIVYPLPREWAHFTGNSTLSNMGLHLAHNKAQWSLL---	417
Db	629	PMCDKHTASVEKSGVGIYIVHPLWETWADLVHPD--AQEILTDTEDNRDWTYSAIRQS	686
Qy	418	---PROHRSRGSSGSG--PDHDHAGQGTSEBEEQ	446
Db	687	PSPPEESRGPHPLPDKQPFELTLEBEEEEE	719
RESULT 11			
	I67946		
	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat		
	N/Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDS4A1		
	N/Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-sp		
	hosphodiesterase RD3)		
	C/Species: Rattus norvegicus (Norway rat)		
	C/Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004		
	C/Accession: I67946; A32558; B32558; C32558		
	R/Bolger, G.B.; Rodgers, L.K.; Riggs, M.		
	Gene 149, 237-244, 1994		
	A/Title: differential CNS expression of alternative mRNA isoforms of the mammalian gene		
	A/Reference number: I53865; MUID:95047482; PMID:7958996		
	A/Accession: I67946		
	A/Status: translated from GB/EMBL/DBJ		
	A/Molecule type: mRNA		
	A/Residues: 1-610 <RES>		
	A/Cross-references: UNIPROT:P54748; UNIPARC:UPI000002A6D4; GB:L27062; NID:G436013; PIDN:		
	R/Davis, R.L.; Takayasu, H.; Eberwine, M.; Myrnes, J.		
	Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989		
	A/Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+) g		
	A/Reference number: A32558; MUID:89264472; PMID:2542942		
	A/Accession: A32558		
	A/Molecule type: mRNA		
	A/Residues: 1-598, 'T', 600-610 <DAV>		
	A/Cross-references: UNIPARC:UPI0000170937; GB:M26715; NID:G203982; PIDN:AAC37699.1; PID:		
	A/Accession: B32558		
	A/Molecule type: mRNA		
	A/Residues: 85-120,154-598, 'T', 600-610 <DA2>		
	A/Cross-references: UNIPARC:UPI0000170939; GB:M26716; GB:M26717; GB:J04554; NID:G203986;		
	A/Note: splice form RD2		
	A/Accession: C32558		
	A/Molecule type: mRNA		
	A/Residues: 26-598, 'T', 600-610 <DA3>		
	A/Cross-references: UNIPARC:UPI0000170938; GB:M26716; NID:G203984; PIDN:AAA41101.1; PID:		
	A/Note: splice form RD3		
	C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'		
	F;14-20/Region: responsible for membrane association		
	F;26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pr		
	F;85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #		
	F;184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>		
	Query Match	23.2%;	Score 559.5; DB 2; Length 610;
	Best Local Similarity	31.1%;	Pred. No. 3.9e-36;
	Matches 133; Conservative	77; Mismatches 163; Indels	55; Gaps 9;
Qy	43	RGSVYPIDFRLNLTSTYSIGTCKKVKRLLSQRYFHASRLLRIGIIPQAPLHLLDEDYL	102
Db	80	RQSQPMVSQITGLKKUUVHTSLNTN-----VPRFGVKTDQEDLL	117
Qy	103	GOARHMLSKVGMWDFDIFLFDRLTNGNSLVTLTCHLFTNTHGLTHFPLKDMVTLHRLFVWV	162



QY 395 NSTLSNMLGHLAHNAQWKSLLPROHRSRGSSGSP-DHDHAGQG-----TE 441  
Db 649 PD--AQDILTLDNR-DW-----YHSATRQSPSPLEEEPGGLHPSLPDKFQFELTL 699  
QY 442 SEEQEGDS 449  
Db 700 EEEEDS 707  
RESULT 13  
S71626  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human  
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase  
C;Species: Homo sapiens (man)  
C;Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: S71626; I61356  
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.  
FEBS Lett. 358, 305-310, 1995  
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific P  
A;Reference number: S71626; MUID:95145731; PMID:7843419  
A;Accession: S71626  
A;Molecule type: DNA  
A;Residues: 1-712 <ENG>  
A;Cross-references: UNIPROT:Q08493; UNIPARC:UPI0000163B31; EMBL:Z46632; NID:9727222; PID:  
A;Experimental source: substantia nigra  
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,  
Mol. Cell. Biol. 13, 6558-6571, 1993  
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memora  
A;Reference number: A54442; MUID:94019330; PMID:8413254  
A;Accession: I61356  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 462-712 <RES>  
A;Cross-references: UNIPARC:UPI000016AE86; GB:L20968; NID:9347125; PIDN:AAA03591.1; PID:  
A;Genetic: HSPD4C1  
C;Function:  
A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP  
A;Pathway: cyclic nucleotide metabolism  
A;Note: expressed in various tissues but not in cells of the immune system  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C;Keywords: phosphoric diester hydrolase  
F;387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
Query Match 23.0%; Score 553; DB 2; Length 712;  
Best Local Similarity 27.8%; Pred. No. 1.6e-35;  
Matches 135; Conservative 94; Mismatches 198; Indels 58; Gaps 10;  
QY 11 EILFENPDQNAKCVCMGLDRLRGQTVRAERRGSYFFDFRLN-----STTVSG-- 61  
Db 204 KLAETLDELWDCLDQLETLQTRHSGVEMASNFKF-----RLNRELTHLSETSRGQ 257  
QY 62 -----EIGTKK-----KVKRLLSQRYFHASRLRGLRGIIPOAPLHLD 99  
Db 258 VSYISRTFLDQTEVPELPKVTAEEAPQMSRISGLHGLCHSASLSATVPREGVQTDQE 317  
QY 100 DYLGQARHMLSKVGMDFDIFLDRLTNGNSLVTLCHLNTGLHIFHFKLDMVTTLHREL 159  
Db 318 EQLAKE--LEDNTKNGLDVFKVADVSGNRPPLTAIFSIQERDLLKTFQIPADTLATYL 374  
QY 160 VMVQEDYHSQNPYHNAVAADVTQAMHCYIKPEKPLASFLTPLDIMGLLAAAHADVDPHG 219  
Db 375 LMLEGHYHANVAVHNSLHAADVAQSTHVLATPALEAVFTDLEITLALFASAIHVDHPG 434  
QY 220 VNQPELTKNHHLANLYQNNSVLNHHHRSSTIGMLRESR--LLAHLPKMTQDIEQQLGS 277  
Db 435 VSNQFLINTNSDALMYNDASVLNHHHLAVGFKLLQACNCDIFQNLAKORLSLRWVID 494  
QY 278 LILATDNRQNEFLTRLKAHLHND-----LLEDAQDRHFMQLKALCADI CNPCRIW 331  
Db 495 MVLATDMSKMHMLADLKTWVETKVTSLGLVLLDYSRDIQVQLNVLHVCADLSNTKPL 554  
QY 332 EMSKQMSERVECEFFYRQGELEQKFELEISPLCNCQKDSIPSIQIGFMSYIPELFREWAH 391

Db 555 PLYRQWTDIMAEFFQGRERESGLDISPMCDKHTASVEKSOVGFDIYIAHLWETWAD 614  
QY 392 FTGNSTLSNMLGHLAHNAQWKSLLPROHRS-RGSSGSGPDH-----DHAGQGTSE 443  
Db 615 LVHPD--AQDLLTLEDNREWTQSKIPSPSLTNPDRGDPDRFQFELTLEAEDEDEE 672  
QY 444 EDEGD 448  
Db 673 EEEGE 677  
RESULT 14  
I67945  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)  
N;Alternate names: cAMP phosphodiesterase 1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I67945; A33904  
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.  
Gene 149, 237-244, 1994  
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes  
A;Reference number: I53865; MUID:95047482; PMID:7958996  
A;Accession: I67945  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-536 <RES>  
A;Cross-references: UNIPROT:P14644; UNIPARC:UPI0000127BF9; GB:L27061; NID:9436011; PIDN:  
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989  
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP  
A;Reference number: A33904; MUID:89315790; PMID:2546153  
A;Accession: A33904  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 230-496 <SWI>  
A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:M28410  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase  
F;253-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
Query Match 22.0%; Score 529.5; DB 2; Length 536;  
Best Local Similarity 30.8%; Pred. No. 7.5e-34;  
Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;  
QY 71 RLISQRYFHASRLRGLRGIIPOAPLHLLDDEYLGQARHMLSKVGMDFDIFLDRLTNGNS 130  
Db 156 QITGLRKSCHTS-LPTAAIPREGVQTDQEQLAKE---LEDNTKNGLDVFKVAELSGNRP 211  
QY 131 LVTLLCHLNTGLHIFHFKLDMVTTLHRLFLVMQVEDYHSQNPYHNAVAADVTQAMHCYIK 190  
Db 212 LTAVIPRVQLERDLLKTFQIPADTLIRYLLTLEGHYSNVAVHNSIHAADVQSAHVLLG 271  
QY 191 EPKLASFLTPLDIMGLLAAAHADVDPHGVNQPELTKNHHLANLYQNNSVLNHHHRSRST 250  
Db 272 TPALEAVFTDLEITLALFASAIHVDHPGVSNQFLINTNSLALMYNDSSVLNHHHLAVG 331  
QY 251 IGMRESR--LLAHLPKMTQDIEQQLGSLLIATDNRQNEFLTRLKAHLHND----- 302  
Db 332 FKLLQACNCDIFQNLAKORLSLRWVIDMLATDMSKMHMLADLKTWVETKVTSLGV 391  
QY 303 LRLEDAQDRHFMQLKALCADI CNPCRIWMSKQMSERVECEFFYRQGELEQKFELEISPL 362  
Db 392 LLLDYSRDIQVQLNVLHVCADLSNPAKPLPLVRQWTERIMAEFFQGRERESGLDISPM 451  
QY 363 CNQCKDSIPSIQIGFMSYIPELFREWAHFTGNSTLSNMLGHLAHNAQWKSLLPROHR 422  
Db 452 CDKHTASVEKSOVGFDIYIAHLWETWADLVHPD--AQELDTLEDNREWTQSRVP---- 505  
QY 423 SRGSSGSGPDH--DHAGQGTSEDEGD 448  
Db 506 CSPHPHAIQDRPKFELTLEETEEDDE 534

```
RESULT 15
T16769
hypothetical protein R153.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16769
R:Kirsten, J.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid R153.
A:Reference number: Z18573
A:Accession: T16769
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-549 <KIR>
A:Cross-references: UNIPROT:Q22000; UNIPARC:UPI000013C0D8; EMBL:U28729; NID:g861238; PID
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R153.1
A:Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
F:281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match      21.5%; Score 517; DB 2; Length 549;
Best Local Similarity 32.6%; Pred. NO. 7.5e-33;
Matches 114; Conservative 72; Mismatches 140; Indels 24; Gaps 6;

QY 105 ARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHHFKLDVTLHRFLVMQOE 164
DB 216 AVHM-QRLDDWGDPVEFKIDELSKNHSLTVTFTSLQRNLKFTFEIHQSTLVTLNLSH 274

QY 165 DYHSQNPYHNAHAAVTOAMCHYCKEPLKAGFLTPDLMGLLAAAHADVDPGVNQPF 224
DB 275 HYRN-NHYNFTHAADVAQSMVLLMSPVLTFTDLEVLAAIFAGAVHDVDPGFTNOY 333

QY 225 LIKTNHHLANLYONMSVLENHHRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILAT 282
DB 334 LINSNNELAIMYNDESVLQHLAVAFKLLQDSNCDFLANLSRKQRLQPKRIVIDWVLAT 393

QY 283 DINRQNEFLTRLKAHLH-----NKDLRLDAQDRHFMLOIALKCADICNPCRIMESKO 336
DB 394 DMSKMSLLADUKTMVEAKKVGNNVIVLDKYNDKIQLQSMIHLADLSNPTKPIELYQQ 453

QY 337 WSERVCEEYFROGELEQFELEISPLCNOQKDSIPSIGFMSYIPEPLFREWAHFTGNS 396
DB 454 WQRIWEEYWRQGDKEKELGLBISPWCDRGNVTIEKSQVGFDIYIVHPLYETWADLVYPD 513

QY 397 TLSENMLGHLAHNAQWKSLLPRQHRSGSGSGSPDHDHAGQGTSEEOE 446
DB 514 --AQNILDQLEENREWYQSRIPE-----EPDTARTVTEDDEHK 549
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Search completed: March 10, 2006, 20:03:03  
Job time : 32.0976 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:25 ; Search time 187.805 Seconds  
(without alignments)  
1690.519 Million cell updates/sec

Title: US-10-781-181-5

Perfect score: 2408

Sequence: 1 MSLVVERCGEILFNPQDN.....PDHAGQCTESEBQGDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2408	100.0	450	1	PDE7B_HUMAN	Q9np56 homo sapien
2	2408	100.0	450	2	Q5VWY9_HUMAN	Q5vwy9 homo sapien
3	2258	93.8	586	2	Q4LE81_HUMAN	Q4le81 homo sapien
4	2192	91.0	446	1	PDE7B_MOUSE	Q9qxl1 mus musculus
5	2178	90.4	446	2	Q8VIE4_RAT	Q8vie4 rattus norv
6	2178	90.4	446	2	Q8CBS2_MOUSE	Q8cbs2 mus musculus
7	2161.5	89.8	459	2	Q8VIE2_RAT	Q8vie2 rattus norv
8	1764	73.3	359	2	Q8VIE3_RAT	Q8vie3 rattus norv
9	1510.5	62.7	456	2	Q4RR95_TETNG	Q4rr95 tetraodon n
10	1425.5	59.2	456	1	PDE7A_MOUSE	P70453 mus musculus
11	1424.5	59.2	482	2	Q6PSG2_MOUSE	Q6psg2 mus musculus
12	1419.5	58.9	482	1	PDE7A_HUMAN	Q13946 homo sapien
13	1418.5	58.9	456	2	Q5R5B5_PONPY	Q5r5b5 pongo pygma
14	1397.5	58.0	436	1	PDE7A_RAT	Q08593 rattus norv
15	1287	53.4	424	2	Q96T72_HUMAN	Q96t72 homo sapien
16	1267.5	52.6	381	2	Q50SM0_XENILA	Q50sm0 xenopus lae
17	1107.5	46.0	324	2	Q4RST4_MACFA	Q4rst4 macaca fasc
18	872	36.2	305	2	Q7PNP5_ANOGA	Q7pnp5 anophelies g
19	711	29.5	199	2	Q4VXJ0_HUMAN	Q4vxj0 homo sapien
20	604.5	25.1	809	1	PDE4D_HUMAN	Q08499 homo sapien
21	603.5	25.1	803	1	PDE4D_RAT	Q14270 rattus norv
22	600.5	24.9	747	1	PDE4D_MOUSE	Q01063 mus musculus
23	580.5	24.1	659	2	Q8VDB1_RAT	Q8vdb1 rattus norv
24	580.5	24.1	721	1	PDE4B_RAT	P14646 rattus norv
25	580.5	24.1	722	2	Q5RKL0_RAT	Q5rkl0 rattus norv
26	580.5	24.1	736	2	Q8VDB2_RAT	Q8vdb2 rattus norv
27	579.5	24.1	691	2	Q4R3J0_TETNG	Q4r3j0 tetraodon n
28	579	24.0	563	2	Q5ZXR6_CHICK	Q5zxr6 gallus gall
29	574.5	23.9	721	2	Q9QX17_MOUSE	Q9qxl7 mus musculus
30	573.5	23.8	503	2	Q6IQY6_MOUSE	Q6iqy6 mus musculus
31	573.5	23.8	542	2	Q91VY2_MOUSE	Q91vy2 mus musculus

32	573.5	23.8	682	2	Q5XGT5_XENILA	Q5xgt5 xenopus lae
33	573.5	23.8	721	2	Q8VBU5_MOUSE	Q8vbu5 mus musculus
34	572	23.8	683	2	Q4SBL4_TETNG	Q4sbl4 tetraodon n
35	568	23.6	867	2	Q4RL51_TETNG	Q4rl51 tetraodon n
36	567.5	23.6	564	2	Q5T3Z8_HUMAN	Q5t3z8 homo sapien
37	567.5	23.6	606	2	Q13945_HUMAN	Q13945 homo sapien
38	567.5	23.6	721	2	Q5VTH5_HUMAN	Q5vth5 homo sapien
39	567.5	23.6	726	2	Q59GM8_HUMAN	Q59gm8 homo sapien
40	567.5	23.6	736	1	PDE4B_HUMAN	Q07343 homo sapien
41	567.5	23.6	736	2	Q5VTH7_HUMAN	Q5vth7 homo sapien
42	565	23.5	647	2	Q8IVA7_HUMAN	Q8iva7 homo sapien
43	565	23.5	825	2	Q9H3H2_HUMAN	Q9h3h2 homo sapien
44	565	23.5	860	2	Q5DM53_HUMAN	Q5dm53 homo sapien
45	565	23.5	864	2	Q6PMT2_HUMAN	Q6pmt2 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	PDE7B_HUMAN	STANDARD;	PRT;	450 AA.
AC	Q9NP56;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).			
GN	Name=PDE7B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;			
RA	Sasaki T., Kotera J., Yuasa K., Omori K.;			
RT	"Identification of human PDE7B, a camp-specific phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 271:575-583(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;			
RA	Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;			
RT	"Cloning and characterization of the human and mouse PDE7B, a novel			
RL	CAMP-specific nucleotide phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 272:186-192(2000).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zengler B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences.";			
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

-!- FUNCTION: May be involved in the control of camp-mediated neural



Db 241 VLENHWRSTIGMLRESLLAHLPKMTQDIEQQGLSLATDINRQNEFLTRLKAHLN 300  
Qy 301 KDLRLAEDQRHFMQLKALCADICNPCIWMSKQMSRVCESFYRQGELEQKFELEIS 360  
Db 301 KDLRLAEDQRHFMQLKALCADICNPCIWMSKQMSRVCESFYRQGELEQKFELEIS 360  
Qy 361 PLCNQKQKDSISIQIGFMSYIPEPLFRWAHFTGNSTLSENMLGHLAHNAQKWSLLPRQ 420  
Db 361 PLCNQKQKDSISIQIGFMSYIPEPLFRWAHFTGNSTLSENMLGHLAHNAQKWSLLPRQ 420  
Qy 421 HRSRSGSGDPDHDHAGQGTSEEGDSP 450  
Db 421 HRSRSGSGDPDHDHAGQGTSEEGDSP 450

RESULT 3  
Q4LE81 HUMAN  
ID Q4LE81 HUMAN PRELIMINARY; PRT; 586 AA.  
AC Q4LE81  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE PDE7B variant protein (fragment).  
GN Name=PDE7B variant protein;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Brain;  
RA Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,  
RA Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;  
RT "Preparation of a set of expression-ready clones of mammalian long  
RT cDNAs encoding large proteins by the ORF trap cloning method."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB209990; BAE06072.1; -; mRNA.  
FT NON TER 1  
SQ SEQUENCE 586 AA; 66230 MW; F96F4F0549A9E8D CRC64;

Query Match 93.8%; Score 2258; DB 2; Length 586;  
Best Local Similarity 100.0%; Pred. No. 2e-166;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDRLRGOTGVAERGSYPIDFRLNSTTYSIGETGKVKVRLLSQRYFHASRLRG 87  
Db 164 GDRLRGOTGVAERGSYPIDFRLNSTTYSIGETGKVKVRLLSQRYFHASRLRG 223  
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGMWDPIFLDRLTNGNSLVTLCHLFTNTHGLIHH 147  
Db 224 IIPQAPLHLLDEYLGQARHMLSKVGMWDPIFLDRLTNGNSLVTLCHLFTNTHGLIHH 283  
Qy 148 FKLDVTLHRLFMVQEDYHSQNPYHNAHADVTQAMHCVLKEPKLASFLTPDIDMGL 207  
Db 284 FKLDVTLHRLFMVQEDYHSQNPYHNAHADVTQAMHCVLKEPKLASFLTPDIDMGL 343  
Qy 208 LAAAHVDVDPGVNPFLLKTNHNLANYQNMSVLENHHRSTIGMLRESLLAHLPKEM 267  
Db 344 LAAAHVDVDPGVNPFLLKTNHNLANYQNMSVLENHHRSTIGMLRESLLAHLPKEM 403  
Qy 268 TDIEEQQLGSLILATDINRQNEFLTRLKAHLNKLRLAEDQRHFMQLKALCADICNP 327  
Db 404 TDIEEQQLGSLILATDINRQNEFLTRLKAHLNKLRLAEDQRHFMQLKALCADICNP 463  
Qy 328 CRIMWSKQMSRVCESFYRQGELEQKFELEISPLCNQKQKDSISIQIGFMSYIPEPLFR 387  
Db 464 CRIMWSKQMSRVCESFYRQGELEQKFELEISPLCNQKQKDSISIQIGFMSYIPEPLFR 523  
Qy 388 EWAHFTGNSTLSENMLGHLAHNAQKWSLLPRQHSRSGSGDPDHDHAGQGTSEEG 447  
Db 524 EWAHFTGNSTLSENMLGHLAHNAQKWSLLPRQHSRSGSGDPDHDHAGQGTSEEG 583

Qy 448 DSP 450  
Db 584 DSP 586

RESULT 4  
PDE7B MOUSE  
ID PDE7B\_MOUSE STANDARD; PRT; 446 AA.  
AC Q9OXQ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE CAMP-specific 3', 5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).  
GN Name=Pde7b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=20087273; PubMed=10618442; DOI=10.1073/pnas.97.1.472;  
RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;  
RT "Cloning and characterization of PDE7B, a CAMP-specific  
RT phosphodiesterase."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J;  
RC MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;  
RA Gardner C.E., Robas N.M., Cawkill D., Fildock M.D.;  
RT "Cloning and characterization of the human and mouse PDE7B, a novel  
RT CAMP-specific nucleotide phosphodiesterase."  
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).  
CC -1- FUNCTION: May be involved in the control of cAMP-mediated neural  
CC activity and cAMP metabolism in the brain.  
CC -1- CATALYTIC ACTIVITY: Adenosine 3', 5'-cyclic phosphate + H(2)O =  
CC adenosine 5'-phosphate.  
CC -1- COFACTOR: Divalent cations (By similarity).  
CC -1- ENZYME REGULATION: Inhibited by diprydamole, IBMX and SCH51866.  
CC Insensitive to zaprinast, rolipram, and milrinone.  
CC -1- PATHWAY: Cyclic nucleotide metabolism.  
CC -1- TISSUE SPECIFICITY: Highly expressed in brain.  
CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two  
CC putative divalent metal sites and an N-terminal regulatory domain.  
CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
CC family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AF190639; AAP25195.1; -; mRNA.  
CC EMBL; AJ251859; CAB92530.1; -; mRNA.  
CC HSSP; Q08499; 10YN.  
CC Ensembl; ENSMUSG00000019990; Mus musculus.  
CC MGI; MGI:1352752; Pde7b.  
CC GO; GO:004115; F:cAMP-specific phosphodiesterase activity; IDA.  
CC InterPro; IPR002073; PDEase.  
CC Pfam; PF00233; PDEase\_1; 1.  
CC PRINTS; PR00387; PDIESTERASE1.  
CC PROSITE; PS00126; PDEASE\_I; 1.  
KW CAMP; Hydrolase.  
.. FT. REGION 172 410 Catalytic (By similarity).  
SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;

Query Match 91.0%; Score 2192; DB 1; Length 446;  
Best Local Similarity 91.6%; Pred. No. 1.9e-161;  
Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

Qy 1 MSLMVERCGEILPENPDQNAKVCMLGDIRLQGTGVAERRGSPIDFRLNSTTYS 60



Db 61 GEIGTKKKVKRLLSFRYFHASRLLRGIIPQAPLHLLDDEYLGQARHMLSKVGTWDFDIF 120  
 QY 121 LFDRLTNGNSLVTLCHLFNTFHTGLIHHFKLDVMVTLHRFLVMVOEDYHSQNPYHNVAHAAD 180  
 Db 121 LFDRLTNGNSLVTLCHLFNSHGLIHHFKLDVMVTLHRFLVMVQEDYGHGNPYHNVAHAAD 180  
 QY 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAADVDVHPGVNQPFLLKTNHHLANLQNMS 240  
 Db 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAADVDVHPGVNQPFLLKTNHHLANLQNMS 240  
 QY 241 VLENHHWRSTIGMLRESRLLAHLPEKMTQDIEQOLGSLLIATDINRQNEFLTRLKAHLN 300  
 Db 241 VLENHHWRSTIGMLRESRLLAHLPEKMTQDIEQOLGSLLIATDINRQNEFLTRLKAHLN 300  
 QY 301 KDLRLDADQRHFMQLQALKCADICNPRIWEMSKQSERVCEFYRQGELEQKFELEIS 360  
 Db 301 KDLRLNVQDRHFMQLQALKCADICNPRIWEMSKQSERVCEFYRQGELEQKFELEIS 360  
 QY 361 PLCNQOKDSIPSIQIGFMSYIVIEPLPREWAHFTGNSTLSNMLGLAHNAKQWKSLLPRQ 420  
 Db 361 PLCNQOKDSIPSIQIGFMTYIVIEPLPREBARFTGNSTLSNMLSHLAHNAKQWKSLLSNQ 420  
 QY 421 HRRSGSGSGPDHHDAGQGTSEEQ-EGDSP 450  
 Db 421 HRRSGS-----QDLGAPAPETLEQTGATP 446  
  
 RESULT 7  
 Q8VIE2\_RAT PRELIMINARY; PRT; 459 AA.  
 AC Q8VIE2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).  
 GN Name=Pde7b; Synonyms=RNPDE7B;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUS=Skeletal muscle;  
 RA Sasaki T., Kotera J., Omori K.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AB057411; BAB79639.1; -, mRNA.  
 DR HSP; Q08499; IOYN.  
 DR Ensembl; ENSRNOG0000013436; Rattus norvegicus.  
 DR RGD; 621016; Pde7b.  
 DR GO; GO:0004114; F.3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.  
 DR GO; GO:0016787; P:hydrolase activity; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR003607; Met\_phos\_hydro.  
 DR InterPro; IPR002073; PDEase.  
 DR Pfam; PF00233; PDEase I; 1.  
 DR PRINTS; PR00387; PDIESTERASE1.  
 DR SMART; SM00471; HDC; 1.  
 DR PROSITE; PS00126; PDEASE\_I; UNKNOWN\_1.  
 KW Hydrolase.  
 SQ SEQUENCE. 459 AA; 52680 MW; A3P26B95C7FC00A5 CRC64;  
  
 Query Match 89.8%; Score 2161.5; DB 2; Length 459;  
 Best Local Similarity 88.1%; Pred. No. 4.5e-159;  
 Matches 409; Conservative 16; Mismatches 20; Indels 19; Gaps 3;  
  
 QY 1 MSCLMYRVCCEILFENPDQNAKVCVCL-----GDRLRGQTGVRAERGSYP 47  
 Db 1 MSCLMYRVCCEILFENPDQNAKVCVCLAA5SPPLPMAGQGVRLRGQTGVPAERGSYP 60  
  
 QY 48 FDFRLLNNTTYSGETGTKKVKRLLSFRYFHASRLLRGIIPQAPLHLLDDEYLGQARH 107  
 Db 61 FDFRLLNNTTYSGETGSKKVKRLLSFRHFHESRLLRGMTPQAPLHLLDDEYLGQARH 120



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QY 108 MLSKVGWMDFDIIEFLDRLTNGNSLVTLCHLFNTHGLIHHFKLDMTVLRHFLVMVQDYH 167
Db 121 MLSKVGWMDFDIIEFLDRLTNGNSLVTLCHLFNTHGLIHHFKLDMTVLRHFLVMVQDYH 180
QY 168 SQNPYHNAHAADVQAMHCYLKEPKLASFLTPDLIMGLGAAAAHVDVHPGVNQPFLLK 227
Db 181 GHPYHNAHAADVQAMHCYLKEPKLASFLTPDLIMGLGAAAAHVDVHPGVNQPFLLK 240
QY 228 TNHHLANLYQNMVLENHHWRSTIGMLRESRLAHLPKEMTDIEQOLGSLIILATDINRQ 287
Db 241 TNHHLANLYQNMVLENHHWRSTIGMLRESRLAHLPKEMTDIEQOLGSLIILATDINRQ 300
QY 288 NEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNPCRHWKSWKSERVCEEFYR 347
Db 301 NEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNPCRHWKSWKSERVCEEFYR 360
QY 348 QGSELEQKFELEISPLCNQKXDSIPSIGIFMSYIVPEPLPREMAHFTGNSTLSENMLGHLA 407
Db 361 QGDLEQKFELEISPLCNQKXDSIPSIGIFMTYIVPEPLPREMAHFTGNSTLSENMLNHLA 420
QY 408 HNKAAQWKSLLPRHRRSGSGSGDPDHAGQGTSESEQ-EGDSP 450
Db 421 HNKAAQWKSLLSNQHRRGSG-----QDPAGTAPETLEQTEGATP 459

RESULT 8
Q8VIE3_RAT PRELIMINARY; PRT; 359 AA.
AC Q8VIE3;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B3 (SC 3.1.4.17).
GN NamesPde7b; Synonyms=RNPE7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Kotera J., Omori K.,
RC TISSUE=Testis;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057410; BAB79638.1; -, mRNA.
DR HSSP; Q08499; 10YN.
DR RGD; 621016; Pde7b.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 359 AA; 41456 MW; 0FF72792737CE48A CRC64;

Query Match 73.3%; Score 1764; DB 2; Length 359;
Best Local Similarity 92.0%; Pred. No. 2.3e-128;
Matches 333; Conservative 7; Mismatches 16; Indels 6; Gaps 2;

QY 90 PQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHHFK 149
Db 3 PQAPLHLLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLFNTHGLIHHFK 62
QY 150 LDMVTLHRLVMVQEDYHSONPVHNAHADVTQAMHCYLKEPKLASFLTPDLIMGLG 209
Db 63 LDMVTLHRLVMVQEDYHGNPVHNAHADVTQAMHCYLKEPKLASFLTPDLIMGLG 122
QY 210 AAAHVDVHPGVNQPFLLKTNHHLANLYQNMVLENHHWRSTIGMLRESRLAHLPKEMTQ 269
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Db 123 AAAHVDVHPGVNQPFLLKTNHHLANLYQNMVLENHHWRSTIGMLRESRLAHLPKEMTQ 182
QY 270 DIEQOLGSLIILATDINRQNEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNPCR 329
Db 183 DIEQOLGSLIILATDINRQNEFLTRLKAHLHNKDLRLDAQDRHFMLOIALKADICNPCR 242
QY 330 IWEMSKQSERVCEEFYRQCELEQKFELEISPLCNQKXDSIPSIGIFMSYIVPEPLPREW 389
Db 243 IWEMSKQSERVCEEFYRQCELEQKFELEISPLCNQKXDSIPSIGIFMTYIVPEPLPREW 302
QY 390 AHFTGNSTLSENMLGHLAHLKAAQWKSLLPRHRRSGSGSGDPDHAGQGTSESEQ-EGD 448
Db 303 ARFTGNSTLSENMLGHLAHLKAAQWKSLLSNQHRRGSG-----QDPAGTAPETLEQTEGA 357
QY 449 SP 450
Db 358 TP 359

RESULT 9
Q4RR95_TETNG PRELIMINARY; PRT; 456 AA.
AC Q4RR95;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome 14 SCAF15003, whole genome shotgun sequence.
DE (fragment).
GN ORFNames=GSTENG00030267001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01015003; CAG09087.1; -, Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 456 456
SQ SEQUENCE 456 AA; 52118 MW; 60B4805381D70669 CRC64;

Query Match 62.7%; Score 1510.5; DB 2; Length 456;
Best Local Similarity 64.5%; Pred. No. 1.4e-108;
Matches 294; Conservative 52; Mismatches 63; Indels 47; Gaps 8;

QY 7 ERCGELTFENPDQNAKVCVML-----GDRL-RQGTGV-RAERGSYP 47
Db 1 QRCGAVTLTSPQNAVQVRMLDRHVDRNRPKHLPAASIAECKLSTGHAGVLLVERGSYP 60
```



QY 48 FIDRLINSTYSGE1--GTTKKVRLLSQRYPHASRLRLGIIPQAP--LHLLDEYLG 103  
 Db 61 LIDLQVLKSSSQGQGEVAGSTFRKQQLSQRYCHASRLRLGIVPHAPLSLHLLDGYLG 120  
 QY 104 QARHMLSKVGMWDFIDFLDRLTNGSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMVQ 163  
 Db 121 QAAHMLSKVGTWDFIDFLDRLTNGSLVTLCHLNFVHGLVHFLQDLMVHLHRLFLGMVQ 180  
 QY 164 EDYHSQNPYNVAAADVTQAMCYLKEPKLASFLTPDLMGLLAAAHDVDPHGVNQ 223  
 Db 181 EDYHSQNPYNVAAADVTQAMCYLKEPKLASFLTPDLMGLLAAAHDVDPHGVNQ 240  
 QY 224 FLTKTHHLLANLY-----QNMVLENHHRSTIGMLRESLLAHLPKEMTQDIEQOLGS 277  
 Db 241 FLTKTHHLLANLY-----QNMVLENHHRSTIGMLRESLLAHLPKEMTQDIEQOLGS 300  
 QY 278 LILATDINRQNEFLTRKLAHLHNKDLRLEDAQDRHFMV-----QIALK 320  
 Db 301 LILATDINRQNEFLTRKLAHLHNKDLRLEDAQDRHFMV-----QIALK 360  
 QY 321 CADICNPCRIMWMSKQWSEVCEEFYRQGELEQKFELEISPLCNQKQSDIPSIGFMSY 380  
 Db 361 CADVCNPCRIMWMSKQWSEVCEEFYRQGELEQKFELEISPLCNQKQSDIPSIGFMSY 419  
 QY 381 IVEPLFREWAFHFCNSTLSENMLGHLAHLNKAQWKS 416  
 Db 420 IVEPLFDEWHFRTEPSPSLRTMNGHLHQNKAWSRL 455

RESULT 10  
 PDE7A\_MOUSE STANDARD; PRT; 456 AA.  
 AC P70453; Q9ERB3;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE High-affinity CAMP-specific 3',5'-cyclic phosphodiesterase 7A  
 DE (SC 3.1.4.17) (P2A).  
 GN Names=Pde7a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=97098542; PubMed=8943082; DOI=10.1073/pnas.93.24.14188;  
 RA Bloom T.J., Beavo J.A.;  
 RT "Identification and tissue-specific expression of PDE7  
 RT phosphodiesterase splice variants."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
 RC TISSUE=Brain, and Testis;  
 RX MEDLINE=20483661; PubMed=11072622; DOI=10.1006/bbr.2000.3613;  
 RA Wang P., Wu P., Egan R.W., Billah M.M.;  
 RT "Cloning, characterization, and tissue distribution of mouse  
 RT phosphodiesterase 7A1."  
 RL Biochem. Biophys. Res. Commun. 276:1271-1277(2000).  
 CC -1- FUNCTION: Plays a role in signal transduction by regulating the  
 CC intracellular concentration of cyclic nucleotides. This  
 CC phosphodiesterase is highly specific for cAMP and may have a role  
 CC in muscle signal transduction.  
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =  
 CC adenosine 5'-phosphate.  
 CC -1- COFACTOR: Divalent cations.  
 CC -1- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.  
 CC -1- PATHWAY: Cyclic nucleotide metabolism.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=PDE7A2;

CC IsoId=P70453-1; Sequence=Displayed;  
 CC Name=2; Synonyms=PDE7A1;  
 CC IsoId=P70453-2; Sequence=VSP\_004594;  
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in the  
 CC skeletal muscle.  
 CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two  
 CC putative divalent metal sites and an N-terminal regulatory domain.  
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
 CC family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; U68171; AAB08479.1; -; mRNA.  
 DR EMBL; AY007702; AAG16295.1; -; mRNA.  
 DR HSSP; Q08499; IOYN.  
 DR Ensembl; ENSMUSG0000019990; Mus musculus.  
 DR MGI; MGI:1202402; Pde7a.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR002073; PDEase.  
 DR Pfam; PF00233; PDEase\_I.1.  
 DR PRINTS; PR00387; PDISTERASE1.  
 DR PROSITE; PS00126; PDEASE\_I.1.  
 KW Alternative splicing; CAMP; Hydrolase.  
 FT REGION 161 425  
 FT VARSPLIC 1 20  
 FT QHVLSSRRGAISFSSSSALFGCPHRLSQ (in isoform  
 FT 2).  
 FT /FTID=VSP\_004594.  
 FT CONFLICT 407 407  
 FT SEQUENCE 456 AA; 52443 MW; 0B826B96490D9F6E CRC64;  
 SQ  
 Query Match 59.2%; Score 1425.5; DB 1; Length 456;  
 Best Local Similarity 62.2%; Pred. No. 5.7e-102;  
 Matches 263; Conservative 71; Mismatches 88; Indels 1; Gaps 1;  
 QY 7 ERCEGLFENPDQNAKVCMLGDIRLGTGVRAERRGSYPFDRLNLTSTYSGEIGTK 66  
 Db 20 KRGAISYDSSDQALYIRMLGDVRSRAGPETERGSHPIDFRIFHSQSDIASVSA 79  
 QY 67 KVKRLLSQRYPHASRLRLGIIPQAPLHLLDEYLGQARHMLSKVGMWDFIDFLDRLT 126  
 Db 80 RNIRLLSFQYRLSRFRGATVCSLDLDEYNGQAKCMLEKVGNNWDFIDFLDRLT 139  
 QY 127 NGNSLVTLCHLNFTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQNPYNVAAADVTQAMH 186  
 Db 140 NGNSLVSLTFHLFSLHGLIEYFHLDMVKLRRLPLVMTQEDYHSQNPYNVAAADVTQAMH 199  
 QY 187 CYLKEPKLASFLTPDLMGLLAAAHDVDPHGVNQPFLLKTNHLLANLYQNMVLENHH 246  
 Db 200 CYLKEPKLASVTPWDILSLANAATHDLDPGVNQPFLLKTNHLLANLYQNMVLENHH 259  
 QY 247 WRSTIGMLRESLLAHLPKEMTQDIPQQLGSLILATDINRQNEFLTRKLAHLNKLRL 306  
 Db 260 WRSVGLLRESGLFSLPLSRQMEAGALILATDISRQNEYLFLSRHLDKGLDHL 319  
 QY 307 DAQDRHFMLOIALKCADICNPCRIMWMSKQWSEVCEEFYRQGELEQKFELEISPLCNQ 366  
 Db 320 DGRHRLVQLMALKCADICNPCRIMWMSKQWSEVCEEFYRQGELEQKFELEISPLCDRQ 379  
 QY 367 KDSIPSIQIGFMSYIVEPLFREWAFHFCNSTLSENMLGHLAHLNKAQWKSLLPRQHSRGS 426  
 Db 380 TTSIANIQIGFMTYLVLEPLFTEWARFSA-TRLSQTMHGLVGLNKAWSKGLORQSPSEDA 438  
 QY 427 SGS 429  
 Db 439 NAA 441

RESULT 11

Qy	247	WRSTIGMLRRESLLAHLPKEMWTQDI	EQOLGSLIILATDINRQNEPLTRLK	KAHLNKHOLRL	308
Db	286	WRSVAGLLRRESGLFSLPESRQEMEA	IGAILIATDISRQNEYL	SLFRSLDKDGLD	345
Qy	307	DAQDRHMLQIALKACADICNPR	TWENSKQWSEVCEEFYRQGELEQK	FELEISPLCNQ	366
Db	346	DGHRHVLQNALKACADICNPR	WNELSKQWSEKTEEFFHQGDIEK	YHGLGVSPCLDRQ	405
Qy	367	KDSTIPSIQIGFMSYIVBPL	FREWAHFTGNSLTSENMLGHLA	HNKAQWKSLLP	426
Db	406	TESIANIQIGFMTYLVPEL	FTEWARFS-DITELSQTMLGHVGL	NKASKWGLQRQ	464
Qy	427	SGS	429		
Db	465	NAA	467		

RESULT 12

PDE7A\_HUMAN

ID

PDE7A\_HUMAN

STANDARD;

PRT;

482 AA.

AC

Q13946;

O15380;

DT

15-JUL-1998

(Rel. 36, Created)

DT

15-JUL-1998

(Rel. 36, Last sequence update)

DT

10-MAY-2005

(Rel. 47, Last annotation update)

DE

High-affinity CAMP-specific 3',5'-cyclic phosphodiesterase 7A

(EC 3.1.4.17) (HCP1) (TM22).

DE

NCBI\_TaxID=9606;

GN

Name=PDE7A;

OS

Homo sapiens (Human).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC

Homo.

OX

NCBI\_TaxID=9606;

RP

[1]

RP

NUCLEOTIDE SEQUENCE (ISOFORM PDE7A1).

RX

MEDLINE=93286141; PubMed=8389765;

RA

Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,

RA

Riggs M., Rodgers L., Beavo J.A., Wigler M.;

RT

"Isolation and characterization of a previously undetected human cAMP

RT

phosphodiesterase by complementation of cAMP phosphodiesterase-

RT

deficient Saccharomyces cerevisiae.";

RL

J. Biol. Chem. 268:12925-12932(1993).

RN

[2]

RP

NUCLEOTIDE SEQUENCE (ISOFORM PDE7A2).

RP

TISSUE=Skeletal muscle;

RC

MEDLINE=97341143; PubMed=9195912; DOI=10.1074/jbc.272.26.16152;

RX

Han P., Zhu X., Michaeli T.;

RA

"Alternative splicing of the high affinity cAMP-specific

RT

phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";

RT

J. Biol. Chem. 272:16152-16157(1997).

CC

-1- FUNCTION: Plays a role in signal transduction by regulating the

CC

intracellular concentration of cyclic nucleotides. This

CC

phosphodiesterase is highly specific for cAMP and may have a role

CC

in muscle signal transduction.

CC

-1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =

CC

adenosine 5'-phosphate.

CC

-1- COFACTOR: Divalent cations.

CC

-1- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.

CC

-1- PATHWAY: Cyclic nucleotide metabolism.

CC

-1- SUBCELLULAR LOCATION: PDE7A1 (57 kDa) is located mostly to soluble

CC

cellular fractions. PDE7A2 (50 kDa) is located to particulate

CC

cellular fractions.

CC

-1- ALTERNATIVE PRODUCTS:

CC

Event=Alternative splicing; Named isoforms=2;

CC

Name=PDE7A1;

CC

Isoid=Q13946-1; Sequence=displayed;

CC

Name=PDE7A2;

CC

Isoid=Q13946-2; Sequence=VSP\_004593;

CC

-1- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal

CC

muscle and at low levels in a variety of tissues including brain

CC

and heart. It is expressed as well in two T-cell lines. PDE7A2 is

CC

found abundantly in skeletal muscle and at low levels in heart.

CC

-1- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2

CC

are found in several fetal tissues, expression is reduced

Query Match	59.2%	Score	1424.5	DB 2	Length	482			
Best Local Similarity	62.2%	Pred. No.	7.3e-102						
Matches	263	Conservative	71	Mismatches	88	Indels	1	Gaps	1
Qy	7	ERCEIEIFENPDQNAKVCMLGDLRLRGQTGVAERGSYPFIDFRLINLSTYSGEIGTK	66						
Db	46	ORRGATSYSDSDQALYIRMLGVDVRSRAGFETERGSHPYIDFRFHSQSDIEASVSA	105						
Qy	67	KVKVRLLSFORYFHASRLLRGIIIPQAPHLHLDDEYLGOARHMLSKVGMWDPIELFRLT	126						
Db	106	RNIRRLLSFORYLSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGWNWNPDIELFRLT	165						
Qy	127	NGNSLVTLCHLFNTHGII.IHHFKLDWTLHRFLWVQEDYHSQNPYHNAVHAADVTQAMH	186						
Db	166	NGNSLVSLTFLHFLSGLGII.EYFLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH	225						
Qy	187	CYLKEPKLASFLTFLDLMGLGIAAAAHVDVHPGVNQPFLLKTNHHLANLYQNMVLENHH	246						
Db	226	CYLKEPKLASVTPWDITLLSLIAAATDLDHPGVNQPFLLKTNHYLATLYQNMVLENHH	285						

34





**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:02:25 ; Search time 40.8537 Seconds  
(without alignments)  
910.666 Million cell updates/sec

Title: US-10-781-181-5  
Perfect score: 2408  
Sequence: 1 MSLMVERCGEILFENPDQN.....PDHAGQGTSESEQSDSP 450

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2258	93.8	502	2	US-09-330-970-1
2	2051	85.2	390	2	US-03-949-016-10020
3	1419.5	58.9	498	1	US-07-688-352C-20
4	1419.5	58.9	498	1	US-08-474-379C-20
5	1419.5	58.9	498	2	US-09-146-249A-20
6	1419.5	58.9	498	2	US-08-206-188B-20
7	1280	53.2	320	2	US-09-330-970-3
8	604.5	25.1	518	2	US-03-602-735B-2
9	604.5	25.1	673	1	US-08-474-379C-63
10	604.5	25.1	673	2	US-09-146-249A-63
11	604.5	25.1	673	2	US-08-206-188B-63
12	603.5	25.1	517	2	US-03-602-735B-4
13	599.5	24.9	673	1	US-08-577-492-35
14	599.5	24.9	673	2	US-09-079-630-35
15	580.5	24.1	562	1	US-07-688-352C-4
16	580.5	24.1	562	1	US-08-942-521B-8
17	580.5	24.1	562	1	US-08-474-379C-4
18	580.5	24.1	562	2	US-09-146-249A-4
19	580.5	24.1	562	2	US-08-206-188B-4
20	580.5	24.1	562	4	PCT-US91-02714-4
21	574.5	23.9	721	2	US-09-983-754-2
22	567.5	23.6	564	1	US-08-577-492-34
23	567.5	23.6	564	1	US-08-942-521B-2
24	567.5	23.6	564	1	US-08-474-379C-59
25	567.5	23.6	564	2	US-08-146-249A-59
26	567.5	23.6	564	2	US-08-206-188B-59
27	567.5	23.6	564	2	US-09-192-702-2

28	567.5	23.6	564	2	US-09-079-630-34	Sequence 34, Appl
29	567.5	23.6	564	2	US-08-445-474-2	Sequence 2, Appl
30	567.5	23.6	564	2	US-09-983-754-4	Sequence 4, Appl
31	567.5	23.6	564	4	PCT-US94-02612-2	Sequence 2, Appl
32	567.5	23.6	736	1	US-07-688-352C-24	Sequence 24, Appl
33	567.5	23.6	736	1	US-08-474-379C-24	Sequence 24, Appl
34	567.5	23.6	736	2	US-09-146-249A-24	Sequence 24, Appl
35	567.5	23.6	736	2	US-08-206-188B-24	Sequence 24, Appl
36	567.5	23.6	736	4	PCT-US91-02714-23	Sequence 23, Appl
37	565	23.5	885	1	US-08-577-492-33	Sequence 33, Appl
38	565	23.5	885	2	US-09-079-630-33	Sequence 65, Appl
39	565	23.5	886	1	US-08-474-379C-65	Sequence 65, Appl
40	565	23.5	886	2	US-09-146-249A-65	Sequence 65, Appl
41	565	23.5	886	2	US-08-206-188B-65	Sequence 65, Appl
42	565	23.5	901	2	US-09-917-254-93	Sequence 9, Appl
43	563	23.4	686	1	US-08-942-521B-9	Sequence 32, Appl
44	562	23.3	606	1	US-08-577-492-32	Sequence 32, Appl
45	562	23.3	606	2	US-09-079-630-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-09-330-970-1  
; Sequence 1, Application US/09330970  
; Patent No. 6146876  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: White, David  
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
; FILE OF INVENTION: Phosphodiesterase  
; FILE REFERENCE: 5800-28  
; CURRENT APPLICATION NUMBER: US/09/330,970  
; CURRENT FILING DATE: 1999-06-11  
; EARLIER APPLICATION NUMBER: 09/277,423  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-330-970-1

Query Match	93.8%	Score 2258;	DB 2;	Length 502;
Best Local Similarity	100.0%	Pred. No. 1.2e-229;		
Matches 423;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	28	GDRLRGQTGVRAERGSYPFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG	87	
Db	80	GDRLRGQTGVRAERGSYPFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG	139	
Qy	88	IIQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFTNTHGLHH	147	
Db	140	IIQAPLHLLDEYLGQARHMLSKVGMWDFDIFDLRLTNGNSLVTLCHLFTNTHGLHH	199	
Qy	148	FKLDVTLHRLFLVWQEDVHSQNPYHNAVHAADVTQAMHCVLKEPKLASFLTPDIDMGL	207	
Db	200	FKLDVTLHRLFLVWQEDVHSQNPYHNAVHAADVTQAMHCVLKEPKLASFLTPDIDMGL	259	
Qy	208	LAAAAHDVHPGVNQPFILIKTNHHLNLYQNMVLENHNRSTIGMLRESLLAHLPKEM	267	
Db	260	LAAAAHDVHPGVNQPFILIKTNHHLNLYQNMVLENHNRSTIGMLRESLLAHLPKEM	319	
Qy	268	TQDIEQGLSLIATDINRQNEFLTRLKAHLHKNDRLEDAQDRHFMQLTALKCADICNP	327	
Db	320	TQDIEQGLSLIATDINRQNEFLTRLKAHLHKNDRLEDAQDRHFMQLTALKCADICNP	379	
Qy	328	CRTWESKQSWSEVCEFEYRQGELEKFELEISPLCNQKDSIPSIQIGFMSVIVEPLFR	387	
Db	380	CRTWESKQSWSEVCEFEYRQGELEKFELEISPLCNQKDSIPSIQIGFMSVIVEPLFR	439	

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QY 388 EWAHFTGNSTLSENMLGHLAHNKAQWKLLPRQHRSRGSGSPDHDHAGQGTSEBEQEG 447
      |||||
Db 440 EWAHFTGNSTLSENMLGHLAHNKAQWKLLPRQHRSRGSGSPDHDHAGQGTSEBEQEG 499
      |||||

QY 448 DSP 450
      |||
Db 500 DSP 502
      |||

RESULT 2
US-09-949-016-10020
; Sequence 10020, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10020
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10020

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US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-688-352C-20

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367	QY	KDSIPSIQIGPWSYIVELPFWNAHFTGNSITLSENMLCHLAHNKAOWKSLIPROHSRGS	426
422	DB	TESIANIQIGPMTYLVLPFLTEWARFS-NTRLSTQMLGHVGLNKAWSKGLQRESSDST	480
427	QY	SGS	429
481	DB	DAA	483

RESULT 4  
US-08-474-379C-20  
; Sequence 20, Application US/08474379C  
; Patent No. 5977305  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED

Query Match	58.9%	Score 1419.5;	DB 1;	Length 498;
Best Local Similarity	61.7%;	Pred.No.5.2e-141;		
Matches 261;	Conservative	70;	Mismatches 91;	Indels 1;
				Gaps 1;

7	ERCGBILFENPDQNAKVCVMGLDRLRGQTGVARRRGSYPFDIFRLLNSTTYSGBIGTK	66
QY	:	
DB	: : : : : :	
62	QRGAISYDSDDTALYIRMLGDVVRVSRAFSESRGGSHPIDFRIFHSQSIEVSVSA	121
QY	:	
DB	: : : : : :	
67	KVKVALLSFQRYFHASRLLRGIIPQAPLHLDELDYLQQAHRMLSKVGMDFDIFLFDRLT	126
QY	:	
DB	: : : : : :	
122	RNIRELLSFQRYLRSSRFPGTAGTVNSNLIIIDDYNGQAICMLEKGVGNWNFDFI	181
QY	:	
DB	: : : : : :	
127	NGNSLVTLCLFNTHGLIHFFHKLDMTWLHRLFVWVOEDYHSQNPPYHNAVHAADVTAQM	186
QY	:	
DB	: : : : : :	

182	Db	NGNSLVSLTFLPSLHGLIEYFFLDDMMKURRFVMTQEDYHSQNPVHNAVAADVTQAH	241
187	Qy	CYLEKPKLASPLTFLDMLGLAAAAHVDHPGVNQPFLLKTNHHLANLYQMSVLENNH	246
242	Db	CYLEKPKLANSVTPWDILLSLIAAAHFDLHPGVNQPFLLKTNHYLATLYKNTSVLENNH	301
247	Qy	WRSTIGMLRSRLAHLPKEMTQDIEQQGLSLILATDINRQNEFTLTKAHUHNKDRLLE	306
302	Db	WRSVAGLLRESGLFSLHPLPESRQOMETQICALITATDISRQNEYLSLFSRSHLDRGDCLLE	361
307	Qy	DAQDRHFMQIATALKKADI CNPCRIWMSKQWSEVCEEYFROGELAEOKFELISPLCNQQ	366
362	Db	DTRRHVLVQALKKADI CNPCRTWELSKQWSEKVTSEFFHQODIEKKYHLGVSPCLDRH	421
367	Qy	KDSIPSIQIGFMSYIVBPLFREWAHFTGNSLTSENMLGHLANXQAKWSLLPQRHRSRGS	426
422	Db	TESTANIQIGFMTYLVPELPTEWARTS-NTRLSTQTMGLHGVGLNKASWKGQLREQSSSBDT	480
427	Qy	SGS	429
481	Db	DAA	483

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RESULT 5
US-09-146-249A-20
; Sequence 20, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
;

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Query Match: 58.9%; Score 1419.5; DB 2; Length 498;  
Best Local Similarity 61.7%; Pred. No. 5.2e-141;  
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERCEILFENPDQNAKVCVCMGDIRLQGTGVAERRGSPYDFPRLNSTTYSGEIGTK 66  
Db 62 QRRGAISSDQATYALYRMLGDRVRVRAGFESRGSHPYIDFRIFHSQSSEIEVSVA 121  
QY 67 KKVRLLSFQRYPHASRLRGIIPOAPLHLDDYLGQARHMLSKVGMWDPDIFLDRLT 126  
Db 122 RNIRRLLSFQRYLRSSRFRGTAVSNSNLIDDDYNGQAKMCKLVGNWNNFDFLDRLT 181  
QY 127 NGNSLVTLCHLNTGHLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMH 186  
Db 182 NGNSLVSLTFPLSLHGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241  
QY 187 CYLKEPKLASFLTPDLIMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNMVLENHH 246  
Db 242 CYLKEPKLANSVTPDWILLSLAAATHDLDPGVNQPFLIKTNHLYLATLYKNTSVLENHH 301  
QY 247 WRSTIGMLRESRLAHLPKEMTQDIEQOLGSLIATDINRQNEFLTRLKAHLHNKDLRL 306  
Db 302 WRSVAGLLRESGLFSLHPLSRQMETQIGALLIATDISRQNEYLSLFRSHLDRGDLCLE 361  
QY 307 DAOHRHFMQLTALKACADICNPRIWMSKOWSERVCEEFYRQGELEKFELEISPLCNOQ 366  
Db 362 DTRHRLHLVQALAKACADICNPCTRWELSKOWSEKVTSEFFHQGDIEKKYHLGVSPLCDRH 421  
QY 367 KDSIPSIQIGFMSYIVPEPLFREWAHFTGNSTLSENMLGHLAHNAQKWSLLPQHRSGS 426  
Db 422 TESTANIQIGFMTYLVPEPLFTWARFS-NTRLSTQMLGHVGLNKAWSKGLQREQSSEDT 480  
QY 427 SGS 429  
Db 481 DAA 483

## RESULT 6

US-08-206-188B-20  
; Sequence 20, Application US/08206188B  
; Patent No. 6100025  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; TITLE OF INVENTION: Processes  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/206,188B  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 498 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-206-188B-20  
Query Match 58.9%; Score 1419.5; DB 2; Length 498;  
Best Local Similarity 61.7%; Pred. No. 5.2e-141;  
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;  
QY 7 ERCEILFENPDQNAKVCVCMGDIRLQGTGVAERRGSPYDFPRLNSTTYSGEIGTK 66  
Db 62 QRRGAISSDQATYALYRMLGDRVRVRAGFESRGSHPYIDFRIFHSQSSEIEVSVA 121  
QY 67 KKVRLLSFQRYPHASRLRGIIPOAPLHLDDYLGQARHMLSKVGMWDPDIFLDRLT 126  
Db 122 RNIRRLLSFQRYLRSSRFRGTAVSNSNLIDDDYNGQAKMCKLVGNWNNFDFLDRLT 181  
QY 127 NGNSLVTLCHLNTGHLIHHFKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMH 186  
Db 182 NGNSLVSLTFPLSLHGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241  
QY 187 CYLKEPKLASFLTPDLIMGLLAAAHDVDPGVNQPFLIKTNHHLANLYQNMVLENHH 246  
Db 242 CYLKEPKLANSVTPDWILLSLAAATHDLDPGVNQPFLIKTNHLYLATLYKNTSVLENHH 301  
QY 247 WRSTIGMLRESRLAHLPKEMTQDIEQOLGSLIATDINRQNEFLTRLKAHLHNKDLRL 306  
Db 302 WRSVAGLLRESGLFSLHPLSRQMETQIGALLIATDISRQNEYLSLFRSHLDRGDLCLE 361  
QY 307 DAOHRHFMQLTALKACADICNPRIWMSKOWSERVCEEFYRQGELEKFELEISPLCNOQ 366  
Db 362 DTRHRLHLVQALAKACADICNPCTRWELSKOWSEKVTSEFFHQGDIEKKYHLGVSPLCDRH 421  
QY 367 KDSIPSIQIGFMSYIVPEPLFREWAHFTGNSTLSENMLGHLAHNAQKWSLLPQHRSGS 426  
Db 422 TESTANIQIGFMTYLVPEPLFTWARFS-NTRLSTQMLGHVGLNKAWSKGLQREQSSEDT 480  
QY 427 SGS 429  
Db 481 DAA 483

## RESULT 7

US-09-330-970-3  
; Sequence 3, Application US/09330970  
; Patent No. 6146876  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: White, David  
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
; TITLE OF INVENTION: Phosphodiesterase  
; FILE REFERENCE: 5800-28  
; CURRENT APPLICATION NUMBER: US/09/330,970  
; CURRENT FILING DATE: 1999-06-11  
; EARLIER APPLICATION NUMBER: 09/277,423  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-330-970-3

Query Match 53.2%; Score 1280; DB 2; Length 320;  
Best Local Similarity 100.0%; Pred. No. 1.4e-126;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 GDRLRGQTGVAERRGSPYDFPRLNSTTYSGEIGTKKKVRLLSFQRYPHASRLRG 87  
Db 80 GDRLRGQTGVAERRGSPYDFPRLNSTTYSGEIGTKKKVRLLSFQRYPHASRLRG 139

QY 88 IIPQAPLHLLDELDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHH 147  
DB 140 IIPQAPLHLLDELDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHH 199  
QY 148 FKLDVMTLHRLVNVQEDYHSQNYHNAHAADVTQAHCHYLKEPKLASFLTPDIDIMGL 207  
DB 200 FKLDVMTLHRLVNVQEDYHSQNYHNAHAADVTQAHCHYLKEPKLASFLTPDIDIMGL 259  
QY 208 LAAAHVDHVGVPQFLIKTNHHLANLYQMSVLEHHWRSTIGMLRESRLLAHLPKEM 267  
DB 260 LAAAHVDHVGVPQFLIKTNHHLANLYQMSVLEHHWRSTIGMLRESRLLAHLPKEM 319  
QY 268 T 268  
DB 320 T 320

RESULT 8  
US-09-602-735B-2  
; Sequence 2, Application US/09602735B  
; Patent No. 6656717  
; GENERAL INFORMATION:  
; APPLICANT: Xin, Xiaonan  
; APPLICANT: Unterbeck, Axel  
; APPLICANT: Hu, Yinghe  
; TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of  
; FILE REFERENCE: 453260-55  
; CURRENT APPLICATION NUMBER: US/09/602,735B  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: U.S. 60/141,196  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-602-735B-2

Query Match 25.1%; Score 604.5; DB 2; Length 518;  
Best Local Similarity 33.3%; Pred. No. 8e-55;  
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLLS----PQRYFHASRLRGIIPQAPLHLLDELDYLGQARHMLSKVGMWDFDIFL 121  
DB 63 KKKVKRPMQISGVKLMHSSLTNSSIPRGVKTQEDVLAKE--LEDVKNKGLHVR 119  
QY 122 FDRLTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLVNVQEDYHSQNYHNAHAAD 180  
DB 120 IAEI-SGNRPLTVIMHTIFQERDILLTKFKIPVDLTILYMTLEDHYHADVAYHNNIHAAD 178  
QY 181 VTQAMHCYLKEPKLASFLTPDIDIMGLAAAHVDHVGVPQFLIKTNHHLANLYQMS 240  
DB 179 VQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQFLINTSELALMYNDSS 238  
QY 241 VLENHWRSTIGMLRES--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFTLRLKAHL 298  
DB 239 VLENHHLAVGFKLQEBNCDFQNLTKKQSLRQKVIDIVLATDMSKHNLLADLKTW 298  
QY 299 HNKD-----LRLEDAQDRHFMLOIALKCADICNPCRIMSKWSKSERVCEEFVROGELE 352  
DB 299 ETKKVTSSGVLDDNYSRDIQVLMVHVCADLSNFTKPLQLYQRTWDRIMEEFPQGDRE 358  
QY 353 QKPLEISPLCNQOKDSIPSIQIFMSYIYVEPLREWAHFTGNSLTSENMLGLAHNAKQ 412  
DB 359 RERGMETSPMCDKGNASVEKSVQGFIDYIYHPLMETWADLVHPD--AQDILDTLEDNREW 416  
QY 413 WKSLLPRQHRSGSGGPDHDHAGQGTSE-----EOEGDS 449  
DB 417 YQSTIPO-----SPSPAPDDPEGRQGTQTEKFOFELTLEDGES 455

RESULT 9  
US-08-474-379C-63  
; Sequence 63, Application US/08474379C  
; Patent No. 5977305  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
; TITLE OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,379C  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/206,188  
; FILING DATE: 01-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,352  
; FILING DATE: 19-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 27866/32771  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-379C-63

Query Match 25.1%; Score 604.5; DB 1; Length 673;  
Best Local Similarity 33.3%; Pred. No. 1.2e-54;  
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLLS----PQRYFHASRLRGIIPQAPLHLLDELDYLGQARHMLSKVGMWDFDIFL 121  
DB 218 KKKVKRPMQISGVKLMHSSLTNSSIPRGVKTQEDVLAKE--LEDVKNKGLHVR 274  
QY 122 FDRLTNGNSLVTLCH-LFNTHGLIHHFKLDVMTLHRLVNVQEDYHSQNYHNAHAAD 180  
DB 275 IAEI-SGNRPLTVIMHTIFQERDILLTKFKIPVDLTILYMTLEDHYHADVAYHNNIHAAD 333  
QY 181 VTQAMHCYLKEPKLASFLTPDIDIMGLAAAHVDHVGVPQFLIKTNHHLANLYQMS 240  
DB 334 VQSTHVLSTPALEAVFTDLEILAAIFASAIHDVDPGVSNQFLINTSELALMYNDSS 393  
QY 241 VLENHWRSTIGMLRES--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFTLRLKAHL 298  
DB 394 VLENHHLAVGFKLQEBNCDFQNLTKKQSLRQKVIDIVLATDMSKHNLLADLKTW 453  
QY 299 HNKD-----LRLEDAQDRHFMLOIALKCADICNPCRIMSKWSKSERVCEEFVROGELE 352  
DB 454 ETKKVTSSGVLDDNYSRDIQVLMVHVCADLSNFTKPLQLYQRTWDRIMEEFPQGDRE 513

Qy 353 QKFELEISPLCNOQKDSIPSQIGFMSYIVPEPLREWAHFTGNSTLSENMLGHLAHNAKQ 412  
Db 514 RERGMEISPMCDKHNASVEKSVQGFIDYIVHPLWETWADLVHPD--AQDILTLEDNREW 571  
Qy 413 WKSLLPQHRSGSGSGPDHDHAGQGTSE-----EQGDS 449  
Db 572 YQSTIPQ-----SPSPAPDDPEGRQGTKEKFQFELTLEDGES 610

## RESULT 10

US-09-146-249A-63  
; Sequence 63, Application US/09146249A  
; Patent No. 6069240  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; NUMBER OF INVENTIONS: Processes  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/146,249A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-146-249A-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;  
Best Local Similarity 33.3%; Pred. No. 1.2e-54;  
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121  
Db 218 KKKRPMSPQISGVKKLHSSSLTNSIPRFGVKTEQEDVLAKL---LEDVKNKGLHVR 274  
Qy 122 FDLTNGNSLVTLCH-LFNTHGLIHFKLDWTLRFLVMVQEDYHSQNPYHNAVHAAD 180  
Db 275 IAEI-SGNRPLTVIMHTIFQERDLKTKFIPVDLTILYMTLEDHYHADYVHNNHAAD 333  
Qy 181 VTQAMHCYKEPKLASFLTPDLMGLAAAAHDVDPGVNQPFLKTNHHLANLYQNM 240  
Db 334 VQSTHVLSTPALEAVFTDLEILAAIPASAIHDVDPGVNQPFLINTSELALMYNDSS 393  
Qy 241 VLENHHRSTIGMLRSR--LLAHLPEKMTQDTEQOLGSLIATDINRQNEFTRUKAHL 298  
Db 394 VLENHHLAVGFKLQENCDIFQNLTKKORSLRKAVDIVLATDMSKIMNLIADLKTWV 453

Qy 299 HNKD-----LRLEDAQDRHFMLOIALKCADICNPKRIWMSKOWSRVCEEFYQGELE 352  
Db 454 ETKKVTSSGVLLDNTSDRIQVQNNWVHCADLSNPKPOLYQWTDIRIMEEFYQGDRE 513  
Qy 353 QKFELEISPLCNOQKDSIPSQIGFMSYIVPEPLREWAHFTGNSTLSENMLGHLAHNAKQ 412  
Db 514 RERGMEISPMCDKHNASVEKSVQGFIDYIVHPLWETWADLVHPD--AQDILTLEDNREW 571  
Qy 413 WKSLLPQHRSGSGSGPDHDHAGQGTSE-----EQGDS 449  
Db 572 YQSTIPQ-----SPSPAPDDPEGRQGTKEKFQFELTLEDGES 610

## RESULT 11

US-08-206-188B-63  
; Sequence 63, Application US/08206188B  
; Patent No. 6100025  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; NUMBER OF INVENTIONS: Processes  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/206,188B  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36107  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-206-188B-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;  
Best Local Similarity 33.3%; Pred. No. 1.2e-54;  
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;  
Qy 66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121  
Db 218 KKKRPMSPQISGVKKLHSSSLTNSIPRFGVKTEQEDVLAKL---LEDVKNKGLHVR 274  
Qy 122 FDLTNGNSLVTLCH-LFNTHGLIHFKLDWTLRFLVMVQEDYHSQNPYHNAVHAAD 180  
Db 275 IAEI-SGNRPLTVIMHTIFQERDLKTKFIPVDLTILYMTLEDHYHADYVHNNHAAD 333  
Qy 181 VTQAMHCYKEPKLASFLTPDLMGLAAAAHDVDPGVNQPFLKTNHHLANLYQNM 240  
Db 334 VQSTHVLSTPALEAVFTDLEILAAIPASAIHDVDPGVNQPFLINTSELALMYNDSS 393





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Qy 182 TQMHCVLKEPKLASFLTPLDIMGLLAAAHVDHFGVNOFPFLIKTNHHLANLYQNMV 241
Db 241 AQSTHVLSTPALDAVFTDLEILAAIFAAAIHVDHFGVSNQFLINTNSELALMYNDES 300
Qy 242 LENHHRSTIGMLRESR--LLAHLPKEMTQDIEOQLGSLIILATDINRQNEFLTELKAHL 299
Db 301 LENHHLAVGFKLQBEHCDIFQNLTKKQRTLRKGVDMVLATDMSKMSLLADLKTWE 360
Qy 300 NKD-----LLEDAQDRHFMLOIALKCADICNPCIWMSKQWSEVCEFYRQGELEQ 353
Db 361 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSILEYRQWTDRIWEEFFQGDKE 420
Qy 354 KFELEISPLCNQKQDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
Db 421 ERGMEISPMCDKHTASVEKQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNW 478
Qy 414 KSLAPR-----QHRSGSSGSGPDHHDH---ACQGTSESEQEGDSP 450
Db 479 QSMIPQSPPPLDERSRDCQGLMEKQFELTLEEDSEGEKEGEP 525

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:18:07 ; Search time 135.976 seconds  
(without alignments)  
1382.771 Million cell updates/sec

Title: US-10-781-181-5  
Perfect score: 2408  
Sequence: 1 MSCLWVERCGEILFENPDQN.....PDHDHAGQGTSEBQCDSP 450

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pdb:  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pdb:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	100.0	450	4	US-10-781-181-5
2	2408	100.0	450	5	US-10-204-268A-2
3	2258	93.8	502	4	US-10-273-517-1
4	2258	93.8	502	4	US-10-386-414-4
5	2258	93.8	502	4	US-10-311-104-1
6	2258	93.8	502	6	US-11-048-744-1
7	2258	93.8	502	6	US-11-048-068-1
8	2192	91.0	446	4	US-10-781-181-1
9	1865	77.5	391	5	US-10-204-268A-4
10	1801	74.8	335	5	US-10-771-833-23
11	1801	74.8	335	5	US-10-886-949-23
12	1430	59.4	288	4	US-10-781-181-3
13	1410.5	58.6	426	3	US-09-966-781A-2
14	1403.5	58.3	426	3	US-09-966-781A-1
15	1397.5	58.0	426	3	US-09-966-781A-3
16	1287	53.4	424	5	US-10-380-437-6
17	1287	53.4	424	5	US-10-380-437-53
18	1286	53.4	432	3	US-09-764-898-208
19	1280	53.2	320	4	US-10-386-414-5
20	1234.5	51.3	334	5	US-10-771-833-22
21	1234.5	51.3	334	5	US-10-886-949-22
22	1194.5	49.6	336	4	US-10-258-746-2
23	771	32.0	211	3	US-09-764-898-280
24	771	32.0	211	3	US-09-989-442-120
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26	604.5	25.1	507	4	US-10-067-514-10
27	604.5	25.1	507	4	US-10-419-723-10

28	604.5	25.1	507	4	US-10-255-120-10
29	604.5	25.1	507	4	US-10-755-889-304
30	604.5	25.1	507	5	US-10-868-397-10
31	604.5	25.1	518	4	US-10-862-722-2
32	604.5	25.1	585	4	US-10-067-514-9
33	604.5	25.1	585	4	US-10-419-723-9
34	604.5	25.1	585	4	US-10-255-120-9
35	604.5	25.1	585	5	US-10-868-397-9
36	604.5	25.1	684	5	US-10-735-973-2
37	604.5	25.1	673	4	US-10-076-597-51
38	604.5	25.1	673	4	US-10-067-514-6
39	604.5	25.1	673	4	US-10-419-723-6
40	604.5	25.1	673	4	US-10-255-120-6
41	604.5	25.1	673	4	US-10-239-439-4
42	604.5	25.1	673	5	US-10-684-206-36
43	604.5	25.1	673	5	US-10-735-973-1
44	604.5	25.1	679	5	US-10-735-973-6
45	604.5	25.1	687	4	US-10-067-514-8

## ALIGNMENTS

## RESULT 1

US-10-781-181-5  
; Sequence 5, Application US/10781181  
; Publication No. US20040137508A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Fidoock, Mark David  
; TITLE OF INVENTION: Enzyme PDE xiv  
; FILE REFERENCE: PC10315B  
; CURRENT APPLICATION NUMBER: US/10781,181  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: GB 9828603.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 09/471,459  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: GB 9922123.6  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Human  
US-10-781-181-5

Query Match					100.0%; Score 2408; DB 4; Length 450;
Best Local Similarity					100.0%; Pred. No. 9.2e-226; Mismatches 0; Indels 0; Gaps 0;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MSCLWVERCGEILFENPDQNAKVCMLGDIRLKGQTVRAERRGSYFFIDFRLINSTTYS	60		
Db	1	MSCLWVERCGEILFENPDQNAKVCMLGDIRLKGQTVRAERRGSYFFIDFRLINSTTYS	60		
Qy	61	GEIGTKKKVRLLSFQRYFPHASRLRGIIIPAPLHLLDELDYLGOARHMLSKVGMWDFDIF	120		
Db	61	GEIGTKKKVRLLSFQRYFPHASRLRGIIIPAPLHLLDELDYLGOARHMLSKVGMWDFDIF	120		
Qy	121	LPRLTNGSLVTLCHLFNTHGLIHFKLDWTLHRLFLVMQVDYHSQPNYHNAHAAD	180		
Db	121	LPRLTNGSLVTLCHLFNTHGLIHFKLDWTLHRLFLVMQVDYHSQPNYHNAHAAD	180		
Qy	181	VTQAMHCYLKPKLASFLTLDIMLGLAAAHDVDPGVNPPILIKTNHHLANLYQMS	240		
Db	181	VTQAMHCYLKPKLASFLTLDIMLGLAAAHDVDPGVNPPILIKTNHHLANLYQMS	240		
Qy	241	VLENHHRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN	300		
Db	241	VLENHHRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN	300		
Qy	301	KDLRLDAQDRHFMQLQIALKCADI CNPCRIWMSKQWSERVCEFFYRQGLEQKFELEIS	360		

Db 301 KDLRLEDAQDRHFMQLKALCADICNPCRIMWMSKQSERVCEFYRQGLEQKFELEIS 360  
Qy 361 PLCNQKQDSTPSIQIGFMSYIVPELFWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
Db 361 PLCNQKQDSTPSIQIGFMSYIVPELFWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
Qy 421 HRSRSGSGGPDHHDAGQGTSEBEQGDSP 450  
Db 421 HRSRSGSGGPDHHDAGQGTSEBEQGDSP 450

## RESULT 2

US-10-204-268A-2  
; Sequence 2, Application US/10204268A  
; Publication No. US20050058647A1  
; GENERAL INFORMATION:  
; APPLICANT: KLUKEN, FRANZ-WERNER  
; APPLICANT: HENTSCH, BERND  
; TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B  
; FILE REFERENCE: MERCK-2484  
; CURRENT APPLICATION NUMBER: US/10/204,268A  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: PCT/EP01/01858  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: EP 00103655.7  
; PRIOR FILING DATE: 2000-02-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-204-268A-2

Query Match 100.0%; Score 2408; DB 5; Length 450;  
Best Local Similarity 100.0%; Pred. No. 9,2e-226;  
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCCEILFENPDQNAKVCMLGDIRLGQGTGVAERGSYPFIDFRLNSTTYS 60  
Db 1 MSCLMVERCCEILFENPDQNAKVCMLGDIRLGQGTGVAERGSYPFIDFRLNSTTYS 60  
Qy 61 GEIGTKKVKRLLSFOFYFHASRLLRGIIIPQAPLHLLDEYLGQARHMLS KVGWDFDIF 120  
Db 61 GEIGTKKVKRLLSFOFYFHASRLLRGIIIPQAPLHLLDEYLGQARHMLS KVGWDFDIF 120  
Qy 121 LPDRLTNGNSLVTLCHLFNTHGLIHFFKLDWVTLHRFLVMVQEDYHSQNPYHNAHAAD 180  
Db 121 LPDRLTNGNSLVTLCHLFNTHGLIHFFKLDWVTLHRFLVMVQEDYHSQNPYHNAHAAD 180  
Qy 181 VTQAMHCYLKEPKLASFLTDLIMGLLAAAHDVDHPGVNQPFLLKTNHHLANLYQNS 240  
Db 181 VTQAMHCYLKEPKLASFLTDLIMGLLAAAHDVDHPGVNQPFLLKTNHHLANLYQNS 240  
Qy 241 VLENHHRSTIGMLRSLLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRKKAHLN 300  
Db 241 VLENHHRSTIGMLRSLLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRKKAHLN 300  
Qy 301 KDLRLEDAQDRHFMQLKALCADICNPCRIMWMSKQSERVCEFYRQGLEQKFELEIS 360  
Db 301 KDLRLEDAQDRHFMQLKALCADICNPCRIMWMSKQSERVCEFYRQGLEQKFELEIS 360  
Qy 361 PLCNQKQDSTPSIQIGFMSYIVPELFWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
Db 361 PLCNQKQDSTPSIQIGFMSYIVPELFWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQ 420  
Qy 421 HRSRSGSGGPDHHDAGQGTSEBEQGDSP 450  
Db 421 HRSRSGSGGPDHHDAGQGTSEBEQGDSP 450

## RESULT 3

US-10-386-414-4

; Sequence 4, Application US/10386414

US-10-273-517-1  
; Sequence 1, Application US/10273517  
; Publication No. US20030143588A1  
; GENERAL INFORMATION:  
; APPLICANT: THORNTON, Michael B.; DING, Li  
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.  
; APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.  
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.  
; APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan  
; APPLICANT: CHAWLA, Narinder K.  
; TITLE OF INVENTION: PHOSPHODIESTERASES  
; FILE REFERENCE: PI-0136 USA  
; CURRENT APPLICATION NUMBER: US/10/273,517  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 60/241,100  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/218,234  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US01/20140  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/213,741  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1  
US-10-273-517-1

Query Match 93.8%; Score 2258; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 4,7e-211;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDRLRGQGTGVAERGSYPFIDFRLNSTTYSGEIGTKKVKRLLSFOFYFHASRLRG 87  
Db 80 GDRLRGQGTGVAERGSYPFIDFRLNSTTYSGEIGTKKVKRLLSFOFYFHASRLRG 139  
Qy 88 IIPQAPLHLLDEYLGQARHMLS KVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLS KVGWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199  
Qy 148 FKLDWVTLHRFLVMVQEDYHSQNPYHNAHAADVTQAMHCYLKEPKLASFLTDLIMGL 207  
Db 200 FKLDWVTLHRFLVMVQEDYHSQNPYHNAHAADVTQAMHCYLKEPKLASFLTDLIMGL 259  
Qy 208 LAAAADVDHPGVNQPFLLKTNHHLANLYQNSVLENHHRSTIGMLRSLLAHLPKEM 267  
Db 260 LAAAADVDHPGVNQPFLLKTNHHLANLYQNSVLENHHRSTIGMLRSLLAHLPKEM 319  
Qy 268 TQDIEQOLGSLILATDINRQNEFLTRKKAHLNKLRLLEDAQDRHFMQLKALCADICNP 327  
Db 320 TQDIEQOLGSLILATDINRQNEFLTRKKAHLNKLRLLEDAQDRHFMQLKALCADICNP 379  
Qy 328 CRIWMSKQSERVCEFYRQGLEQKFELEISPLCNQKQDSTPSIQIGFMSYIVPELFR 387  
Db 380 CRIWMSKQSERVCEFYRQGLEQKFELEISPLCNQKQDSTPSIQIGFMSYIVPELFR 439  
Qy 388 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPQHRSRSGSGGPDHHDAGQGTSEBEQEG 447  
Db 440 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPQHRSRSGSGGPDHHDAGQGTSEBEQEG 499  
Qy 448 DSP 450  
Db 500 DSP 502

## RESULT 4

US-10-386-414-4

; Sequence 4, Application US/10386414

```
Publication No. US20040006016A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Meyers, Rachel E.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
55052 AND 10218 MOLECULES AND USES THEREFOR
FILE REFERENCE: ME103-0210NMIM
CURRENT APPLICATION NUMBER: US/10/386,414
CURRENT FILING DATE: 2003-03-11
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/426,282
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/668,266
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/330,970
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 09/724,599
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/860,193
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 10/283,023
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,044
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/010,943
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/254,037
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/833,082
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
TYPE: PRT
ORGANISM: Homo Sapien
US-10-386-414-4

Query Match 93.8%; Score 2258; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.7e-211;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVARRRGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87
Db 80 GDIRLRGQTGVARRRGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFDRLTNGNSLVTLCHLFNTHGLIHH 147
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFDRLTNGNSLVTLCHLFNTHGLIHH 199
Qy 148 FKLDMTVTLHRLFLVMVQSDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGL 207
Db 200 FKLDMTVTLHRLFLVMVQSDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGL 259
Qy 208 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMVLENNHWRSTIGMLRESRLLAHLPEM 267
Db 260 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMVLENNHWRSTIGMLRESRLLAHLPEM 319
Qy 268 TDIEQQLGSLILATDINRQNEFLTRLKAHLNKLRLLEDAQDRHFMLOIALKCADICNP 327
Db 320 TDIEQQLGSLILATDINRQNEFLTRLKAHLNKLRLLEDAQDRHFMLOIALKCADICNP 379
Qy 328 CRIWEMSKQSERVCEBFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVEPLFR 387
Db 380 CRIWEMSKQSERVCEBFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVEPLFR 439
Qy 388 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPROHRSRGSGSGDPDHDHAGGTSEBQEG 447

Db 440 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPROHRSRGSGSGDPDHDHAGGTSEBQEG 499
Qy 448 DSP 450
Db 500 DSP 502

RESULT 5
US-10-311-104-1
Sequence 1, Application US/10311104
Publication No. US20040054138A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: THORNTON, Michael
APPLICANT: DING, Li
APPLICANT: ARIVU Chandra S.
APPLICANT: YAO, Monique G.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: LAL, Preeti G.
APPLICANT: HAPALIA, April J. A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: LU, Yan
APPLICANT: Chawla, Narinder K.
TITLE OF INVENTION: PHOSPHODIESTERASES
FILE REFERENCE: PI-0136 PCT
CURRENT APPLICATION NUMBER: US/10/311,104
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: PCT/US01/20140
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,741
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/218,234
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/241,100
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 502
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
US-10-311-104-1

Query Match 93.8%; Score 2258; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.7e-211;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVARRRGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87
Db 80 GDIRLRGQTGVARRRGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFDRLTNGNSLVTLCHLFNTHGLIHH 147
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFDI FLFDRLTNGNSLVTLCHLFNTHGLIHH 199
Qy 148 FKLDMTVTLHRLFLVMVQSDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGL 207
Db 200 FKLDMTVTLHRLFLVMVQSDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGL 259
Qy 208 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMVLENNHWRSTIGMLRESRLLAHLPEM 267
Db 260 LAAAAHDVDHPGVNQPFLLKTNHHLANLYQNMVLENNHWRSTIGMLRESRLLAHLPEM 319
Qy 268 TDIEQQLGSLILATDINRQNEFLTRLKAHLNKLRLLEDAQDRHFMLOIALKCADICNP 327
Db 320 TDIEQQLGSLILATDINRQNEFLTRLKAHLNKLRLLEDAQDRHFMLOIALKCADICNP 379
Qy 328 CRIWEMSKQSERVCEBFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVEPLFR 387
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Db 380 CRIWMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVBPLFR 439  
Qy 388 EWAHFTGNSTLSNMLGHLAHNKAQWKSLLPROHRSRGSSGSGPDHHDHAGQGTSESEBQEG 447  
Db 440 EWAHFTGNSTLSNMLGHLAHNKAQWKSLLPROHRSRGSSGSGPDHHDHAGQGTSESEBQEG 499  
Qy 448 DSP 450  
Db 500 DSP 502

## RESULT 6

US-11-048-744-1  
; Sequence 1, Application US/11048744  
; Publication No. US20050164275A1  
; GENERAL INFORMATION:  
; APPLICANT: THORNTON, Michael B.; DING, Li  
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.  
; APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.  
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.  
; APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan  
; APPLICANT: CHAWLA, Narinder K.  
; TITLE OF INVENTION: PHOSPHODIESTERASES  
; FILE REFERENCE: PI-0136 USA  
; CURRENT APPLICATION NUMBER: US/11/048,744  
; CURRENT FILING DATE: 2005-02-03  
; PRIOR APPLICATION NUMBER: US/10/273,517  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 60/241,100  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/218,234  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US01/20140  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/213,741  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7476201CD1  
US-11-048-744-1

Query Match 93.8%; Score 2258; DB 6; Length 502;  
Best Local Similarity 100.0%; Pred. No. 4.7e-211;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 28 GDRLRGQTGVRAERRGSYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87  
Db 80 GDRLRGQTGVRAERRGSYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139  
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199  
Qy 148 FKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLIMLGL 207  
Db 200 FKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLIMLGL 259  
Qy 208 LAAAAHDVHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319  
Qy 268 TDIEQOLGSLILATDINRQNEFLTRLKAHLNKKDLREDAQDRHFMQLIALKCADICNP 327  
Db 320 TDIEQOLGSLILATDINRQNEFLTRLKAHLNKKDLREDAQDRHFMQLIALKCADICNP 379  
Qy 328 CRIWMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVBPLFR 387

Db 380 CRIWMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVBPLFR 439  
Qy 388 EWAHFTGNSTLSNMLGHLAHNKAQWKSLLPROHRSRGSSGSGPDHHDHAGQGTSESEBQEG 447  
Db 440 EWAHFTGNSTLSNMLGHLAHNKAQWKSLLPROHRSRGSSGSGPDHHDHAGQGTSESEBQEG 499  
Qy 448 DSP 450  
Db 500 DSP 502

## RESULT 7

US-11-048-068-1  
; Sequence 1, Application US/11048068  
; Publication No. US20050202478A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: THORNTON, Michael  
; APPLICANT: DING, Li  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: YAO, Monique G.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: LAL, Preeti  
; APPLICANT: HAFALIA, April J. A.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: LU, Yan  
; APPLICANT: WALIA, Narinder K.  
; TITLE OF INVENTION: PHOSPHODIESTERASES  
; FILE REFERENCE: PI-0136 PCT  
; CURRENT APPLICATION NUMBER: US/11/048,068  
; CURRENT FILING DATE: 2005-02-02  
; PRIOR APPLICATION NUMBER: 60/213,741  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7476201CD1  
US-11-048-068-1

Query Match 93.8%; Score 2258; DB 6; Length 502;  
Best Local Similarity 100.0%; Pred. No. 4.7e-211;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 28 GDRLRGQTGVRAERRGSYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87  
Db 80 GDRLRGQTGVRAERRGSYFFIDFRLNLSNTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139  
Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199  
Qy 148 FKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLIMLGL 207  
Db 200 FKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLIMLGL 259  
Qy 208 LAAAAHDVHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319  
Qy 268 TDIEQOLGSLILATDINRQNEFLTRLKAHLNKKDLREDAQDRHFMQLIALKCADICNP 327  
Db 320 TDIEQOLGSLILATDINRQNEFLTRLKAHLNKKDLREDAQDRHFMQLIALKCADICNP 379  
Qy 328 CRIWMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVBPLFR 387  
Db 380 CRIWMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVBPLFR 439

Qy 388 EWAHFTGNSTLSENMLGHLAANKAOWKSLLPQHRSGSGSGDPDHDHAGQGTSEBQEG 447  
Db 440 EWAHFTGNSTLSENMLGHLAANKAOWKSLLPQHRSGSGSGDPDHDHAGQGTSEBQEG 499  
Qy 448 DSP 450  
Db 500 DSP 502

## RESULT 8

US-10-781-181-1  
; Sequence 1, Application US/10781181  
; Publication No. US20040137508A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Fideck, Mark David  
; TITLE OF INVENTION: Enzyme PDE xiv  
; FILE REFERENCE: PCI0315B  
; CURRENT APPLICATION NUMBER: US/10781,181  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: GB 9828603.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 09/471,459  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: GB 9922123.6  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Mouse  
US-10-781-181-1

Query Match 91.0%; Score 2192; DB 4; Length 446;  
Best Local Similarity 91.6%; Pred. No. 1.1e-204;  
Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;  
Qy 1 MSCLMVERCGEILFENPDQAKVCMLGDIIRLQGTGVRAERRSGYFPDFRLNNTYS 60  
Db 1 MSCLMVERCGEVLFPESQSKVCMLGDLVLRQGTGPAERRSGYFPDFRLNNTHS 60  
Qy 61 GEIGTKKKVKLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDPDIF 120  
Db 61 GEIGTKKKVKLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDPDIF 120  
Qy 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
Db 121 LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNPYHNAVAAD 180  
Qy 181 VTQAMHCYKPEKPLASFLTPDIDMLGLLAAAHDVDHGVNQPFLIKTNHLANLYQNS 240  
Db 181 VTQAMHCYKPEKPLASFLTPDIDMLGLLAAAHDVDHGVNQPFLIKTNHLANLYQNS 240  
Qy 241 VLENHWRSTIGMLRESRLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN 300  
Db 241 VLENHWRSTIGMLRESRLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLN 300  
Qy 301 KDLREDAQDRHFMQLQALKADICNPCRIMWMSKQSERVCEEFYRQGELEOKFELEIS 360  
Db 301 KDLREDAQDRHFMQLQALKADICNPCRIMWMSKQSERVCEEFYRQGELEOKFELEIS 360  
Qy 361 PLCNQKQKDSIPSIQIGFMSYIVLPELFWHNAHFTGNSTLSENMLGHLAANKAOWKSLLPQ 420  
Db 361 PLCNQKQKDSIPSIQIGFMSYIVLPELFWHNAHFTGNSTLSENMLGHLAANKAOWKSLLPQ 420  
Qy 421 HRSRSGSGDPDHDHAGQGTSEBQEGDSP 450  
Db 421 HRRSGG-----QDLGAPETLQGTGATP 446

## RESULT 9

US-10-204-268A-4  
; Sequence 4, Application US/10204268A  
; Publication No. US20050058647A1  
; GENERAL INFORMATION:  
; APPLICANT: KLUXEN, FRANZ-WERNER  
; APPLICANT: HENTSCH, BERND  
; TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B  
; FILE REFERENCE: MERCK-2484  
; CURRENT APPLICATION NUMBER: US/10/204,268A  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: PCT/EP01/01858  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: EP 00103655.7  
; PRIOR FILING DATE: 2000-02-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (188)  
; OTHER INFORMATION: Pro or His  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (387)  
; OTHER INFORMATION: Val, Ala, Asp, Glu or Gly  
US-10-204-268A-4

Query Match 77.5%; Score 1865; DB 5; Length 391;  
Best Local Similarity 92.7%; Pred. No. 7.4e-173;  
Matches 354; Conservative 2; Mismatches 26; Indels 0; Gaps 0;  
Qy 52 RLNSTTYSGEIGTKKKVKLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 111  
Db 10 RLNSTTYSGEIGTKKKVKLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 69  
Qy 112 VGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNP 171  
Db 70 VGMWDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRLFLVMVQEDYHSQNP 129  
Qy 172 YHNAVAADVTQAMHCYKPEKPLASFLTPDIDMLGLLAAAHDVDHGVNQPFLIKTNH 231  
Db 130 YHNAVAADVTQAMHCYKPEKPLASFLTPDIDMLGLLAAAHDVDHGVNQPFLIKTNH 189  
Qy 232 LANLYQNSVLENHWRSTIGMLRESRLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 291  
Db 190 LANLYQNSVLENHWRSTIGMLRESRLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 249  
Qy 292 TRLKAHLHNNKDLREDAQDRHFMQLQALKADICNPCRIMWMSKQSERVCEEFYRQGE 351  
Db 250 TRLKAHLHNNKDLREDAQDRHFMQLQALKADICNPCRIMWMSKQSERVCEEFYRQGE 309  
Qy 352 EQKFELEISPLCNQKQKDSIPSIQIGFMSYIVLPELFWHNAHFTGNSTLSENMLGHLAANKA 411  
Db 310 EQKFELEISPLCNQKQKDSIPSIQIGFMSYIVLPELFWHNAHFTGNSTLSENMLGHLAANKA 369  
Qy 412 QWKSLLPQHRSGSGSGDPD 433  
Db 370 QWKSLLPSSTEAGAAALXGLDH 391

## RESULT 10

US-10-771-833-23  
; Sequence 23, Application US/10771833  
; Publication No. US20050048573A1  
; GENERAL INFORMATION:  
; APPLICANT: MILBURN, MICHAEL V.  
; TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES  
; FILE REFERENCE: 039363-1106  
; CURRENT APPLICATION NUMBER: US/10/771,833  
; CURRENT FILING DATE: 2004-02-03

```
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: 60/444,734
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-833-23

Query Match      74.8%; Score 1801; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLNFTHGLIH 146
Db 1 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLNFTHGLIH 60

Qy 147 HFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMIG 206
Db 61 HFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMIG 120

Qy 207 LLA AAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 266
Db 121 LLA AAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 180

Qy 267 MTODIEQOGLSLILATDINRQNEFLTRLKAHLNKKDLRLLEDAQRHFMLOIALKCADICN 326
Db 181 MTODIEQOGLSLILATDINRQNEFLTRLKAHLNKKDLRLLEDAQRHFMLOIALKCADICN 240

Qy 327 PCRIWMSKQWSRVCEEFYRQGELEQKFELEISPLCNQOKDSIPSTIQIGFMSYIIVEPLF 386
Db 241 PCRIWMSKQWSRVCEEFYRQGELEQKFELEISPLCNQOKDSIPSTIQIGFMSYIIVEPLF 300

Qy 387 REWAHFTGNTSLSENMLGHLAHNKAQWKSLLPRQH 421
Db 301 REWAHFTGNTSLSENMLGHLAHNKAQWKSLLPRQH 335

RESULT 11
US-10-886-949-23
; Sequence 23, Application US/10886949
; Publication No. US20050079548A1
; GENERAL INFORMATION:
; APPLICANT: DEAN R. ARTIS
; APPLICANT: BOLLAG, GIDSON
; APPLICANT: CARD, GRAHAM
; APPLICANT: MARTIN, FERNANDO
; APPLICANT: MILBURN, MICHAEL V.
; APPLICANT: ZHANG, KAM
; TITLE OF INVENTION: PDEA CRYSTAL STRUCTURE AND USES
; FILE REFERENCE: 039363-1108
; CURRENT APPLICATION NUMBER: US/10/886,949
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-949-23

Query Match      74.8%; Score 1801; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLNFTHGLIH 146
Db 1 GIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCHLNFTHGLIH 60

Qy 147 HFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMIG 206
Db 61 HFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDLMIG 120

Qy 207 LLA AAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 266
Db 121 LLA AAAHDVDHPGVNQPFLLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPK 180

Qy 267 MTODIEQOGLSLILATDINRQNEFLTRLKAHLNKKDLRLLEDAQRHFMLOIALKCADICN 326
Db 181 MTODIEQOGLSLILATDINRQNEFLTRLKAHLNKKDLRLLEDAQRHFMLOIALKCADICN 240

Qy 327 PCRIWMSKQWSRVCEEFYRQGELEQKFELEISPLCNQOKDSIPSTIQIGFMSYIIVEPLF 386
Db 241 PCRIWMSKQWSRVCEEFYRQGELEQKFELEISPLCNQOKDSIPSTIQIGFMSYIIVEPLF 300

Qy 387 REWAHFTGNTSLSENMLGHLAHNKAQWKSLLPRQH 421
Db 301 REWAHFTGNTSLSENMLGHLAHNKAQWKSLLPRQH 335

RESULT 12
US-10-781-181-3
; Sequence 3, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: FIDOCK, MARK DAVID
; TITLE OF INVENTION: Enzyme PDE xiv
; FILE REFERENCE: PC10315B
; CURRENT APPLICATION NUMBER: US/10/781,181
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: GB 9828603.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/471,459
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 9922123.6
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Human
US-10-781-181-3

Query Match      59.4%; Score 1430; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-130;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVRCGEILFENPDQNAKVCVCMGLDIRLGQTGVRAERGSYPFIDFRLNSTTYS 60
Db 1 MSCLMVRCGEILFENPDQNAKVCVCMGLDIRLGQTGVRAERGSYPFIDFRLNSTTYS 60

Qy 61 GEIGTKKVKRLLSFOFYFHASRLRGIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIF 120
Db 61 GEIGTKKVKRLLSFOFYFHASRLRGIIPQAPLHLLDDEYLGQARHMLSKVGMWDFDIF 120

Qy 121 LFDRLTNGNSLVTLCHLNFTHGLIHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
Db 121 LFDRLTNGNSLVTLCHLNFTHGLIHFKLDWVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPDLMIGLLAAAHADVDPGVNQPFLLIKTNHHLANLYQNMS 240
Db 181 VTQAMHCYLKEPKLASFLTPDLMIGLLAAAHADVDPGVNQPFLLIKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 13
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US-09-966-781A-2  
; Sequence 2, Application US/09966781A  
; Publication No. US20030036184A1  
; GENERAL INFORMATION:  
; APPLICANT: SOULARD, PATRICIA  
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR  
; FILE REFERENCE: A000281US  
; CURRENT APPLICATION NUMBER: US/09/966, 781A  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP004026837  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-966-781A-2

Query Match 58.6%; Score 1410.5; DB 3; Length 426;  
Best Local Similarity 63.1%; Pred. No. 1.9e-128;  
Matches 260; Conservative 67; Mismatches 84; Indels 1; Gaps 1;

QY 18 DONAKVCMLGDIIRLQGTGVRARRGSGSYFIDFRLNLTSTYSGEIGTKKKVKRLLSFOR 77  
DB 1 DOTALYIRMLGDIIVRVRAGFETERRGSHPYIDFRIHFSQSDIEASVSARNIRLLSFOR 60  
QY 78 YFHASRLRLGIIPOAPLHLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCH 137  
DB 61 YLRSSFRFGATVCSNLDLDEYNGQAKMELKVGWNNDFDIFLDRLTNGNSLVSLTFH 120  
QY 138 LFNTGHLIHFKLDVMTLHRLVQVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASF 197  
DB 121 LFSLHGLIEYFHLDMVKLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLAS 180  
QY 198 LTPDLIMGLLAAAHDVDPHGVNQPFLIKTNHHLANLYQNMVLENHNRSTIGMLRES 257  
DB 181 VTPWDILLSIAAATHDLDHPGVNQPFLIKTNHLYLATLYKNTSVLENHNRSAVGLLRES 240  
QY 258 RLLAHLPKEMTQDIEQOLGSLIATDINRQNEFLTRKAHLHNKDLRLDAQDRHFMLOI 317  
DB 241 GLFSHLPLESRQMEAGIILATDISRQNEVLSLFRSHLDKGLDLDGRHRLVLMQ 300  
QY 318 ALKADICNCPRIWEMSKQWSEVCEFYRQGELEISPLCNOQKDSIPSIQIGF 377  
DB 301 ALKADICNCPRIWEMSKQWSEVCEFYRQGELEISPLCNOQKDSIPSIQIGF 360  
QY 378 MSYIVPLFREWAFHTGNSLTSENMLGHLAHNKAQWKSLLPQHRSRGSGS 429  
DB 361 MTYLVEPLFEWARFSA-TRLSQTMGLGVGLINKASWKGLOQPSPSEDANAA 411

RESULT 14  
US-09-966-781A-1  
; Sequence 1, Application US/09966781A  
; Publication No. US20030036184A1  
; GENERAL INFORMATION:  
; APPLICANT: SOULARD, PATRICIA  
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR  
; FILE REFERENCE: A000281US  
; CURRENT APPLICATION NUMBER: US/09/966, 781A  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP004026837  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-966-781A-1

Query Match 58.3%; Score 1403.5; DB 3; Length 426;  
Best Local Similarity 62.6%; Pred. No. 9.1e-128;  
Matches 258; Conservative 66; Mismatches 87; Indels 1; Gaps 1;

QY 18 DONAKVCMLGDIIRLQGTGVRARRGSGSYFIDFRLNLTSTYSGEIGTKKKVKRLLSFOR 77  
DB 1 DOTALYIRMLGDIIVRVRAGFETERRGSHPYIDFRIHFSQSEIEVSVSARNIRLLSFOR 60  
QY 78 YFHASRLRLGIIPOAPLHLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCH 137  
DB 61 YLRSSFRFGATVCSNLDLDEYNGQAKMELKVGWNNDFDIFLDRLTNGNSLVSLTFH 120  
QY 138 LFNTGHLIHFKLDVMTLHRLVQVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASF 197  
DB 121 LFSLHGLIEYFHLDMVKLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLAS 180  
QY 198 LTPDLIMGLLAAAHDVDPHGVNQPFLIKTNHHLANLYQNMVLENHNRSTIGMLRES 257  
DB 181 VTPWDILLSIAAATHDLDHPGVNQPFLIKTNHLYLATLYKNTSVLENHNRSAVGLLRES 240  
QY 258 RLLAHLPKEMTQDIEQOLGSLIATDINRQNEFLTRKAHLHNKDLRLDAQDRHFMLOI 317  
DB 241 GLFSHLPLESRQMEAGIILATDISRQNEVLSLFRSHLDKGLDLDGRHRLVLMQ 300  
QY 318 ALKADICNCPRIWEMSKQWSEVCEFYRQGELEISPLCNOQKDSIPSIQIGF 377  
DB 301 ALKADICNCPRIWEMSKQWSEVCEFYRQGELEISPLCNOQKDSIPSIQIGF 360  
QY 378 MSYIVPLFREWAFHTGNSLTSENMLGHLAHNKAQWKSLLPQHRSRGSGS 429  
DB 361 MTYLVEPLFEWARFSA-NTRLSQTMGLGVGLINKASWKGLOQBOSSEDANAA 411

RESULT 15  
US-09-966-781A-3  
; Sequence 3, Application US/09966781A  
; Publication No. US20030036184A1  
; GENERAL INFORMATION:  
; APPLICANT: SOULARD, PATRICIA  
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR  
; FILE REFERENCE: A000281US  
; CURRENT APPLICATION NUMBER: US/09/966, 781A  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP004026837  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-966-781A-3

Query Match 58.0%; Score 1397.5; DB 3; Length 426;  
Best Local Similarity 62.4%; Pred. No. 3.5e-127;  
Matches 257; Conservative 68; Mismatches 86; Indels 1; Gaps 1;

QY 18 DONAKVCMLGDIIRLQGTGVRARRGSGSYFIDFRLNLTSTYSGEIGTKKKVKRLLSFOR 77  
DB 1 DOTALYIRMLGDIIVRVRAGFETERRGSHPYIDFRIHFSQSEIEVSVSARNIRLLSFOR 60  
QY 78 YFHASRLRLGIIPOAPLHLDEYLGQARHMLSKVGMWDFDIFLDRLTNGNSLVTLCH 137  
DB 61 YLRSSFRFGATVCSNLDLDEYNGQAKMELKVGWNNDFDIFLDRLTNGNSLVSLTFH 120  
QY 138 LFNTGHLIHFKLDVMTLHRLVQVQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLASF 197  
DB 121 LFSLHGLIEYFHLDMVKLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLAS 180  
QY 198 LTPDLIMGLLAAAHDVDPHGVNQPFLIKTNHHLANLYQNMVLENHNRSTIGMLRES 257

Db	181	VTPWDILLSLIAAATHOLDHFGVNQPELIKTNNHYLATLYKNTSVLENHHWRSVAGLLRES	240
Qy	258	RLLAHLPEKEMTODIEQQQLGSLILATDINRQNEFLTRIKAHLNKDLLEDAQDRHFMLQI	317
Db	241	GLFSHLPLESRHEWEAQIGALILATDISRQNEYLSPFRSHLDKGDHLDDGRHRLVLQM	300
Qy	318	ALKCADICNPCRIMWSKQSERVCEEFYRQGELEQKFELEISPLCNQOKDSIPSIQIGF	377
Db	301	ALKCADICNPCRINWELSKQSEKVTSEFFHQGDIEKKYHLGVSPCLCDRQTESIANIQIGF	360
Qy	378	MSYIVEPLPREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPROHRSRGSSGS	429
Db	361	MTYLQEPFTTEWARFS-DTRLSTQMLGHVGLNKASWKGLQROQPSSEDASAA	411

Search completed: March 10, 2006, 20:22:34  
Job time : 136.976 secs



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QM protein - protein search, using sw model

Run on: March 10, 2006, 20:19:01 ; Search time 17.6829 Seconds  
(without alignments)  
708.350 Million cell updates/sec

Title: US-10-781-181-5  
Perfect score: 2408  
Sequence: 1 MSLMVERGCEILLFENPDQN.....PDHAGQGTSESEQEDSP 450

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
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2: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pdb.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pdb.\*  
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8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2258	93.8	502	7	US-11-226-701-4
2	1280	53.2	320	7	US-11-226-701-6
3	604.5	25.1	507	7	US-11-091-018-10
4	604.5	25.1	585	7	US-11-091-018-9
5	604.5	25.1	673	7	US-11-091-018-6
6	604.5	25.1	687	7	US-11-091-018-8
7	604.5	25.1	745	7	US-11-091-018-4
8	604.5	25.1	748	6	US-10-492-835-12
9	604.5	25.1	748	6	US-10-492-835-28
10	604.5	25.1	809	7	US-11-091-018-2
11	603.5	25.1	747	6	US-10-492-835-8
12	603.5	25.1	747	6	US-10-492-835-27
13	594.5	24.7	747	6	US-10-492-835-15
14	570.5	23.7	736	7	US-11-123-893-13
15	567.5	23.6	736	7	US-11-169-041-207
16	556.5	23.1	398	7	US-11-123-893-11
17	546.5	22.7	357	7	US-11-123-893-12
18	448.5	18.6	769	7	US-11-072-512-2646
19	298	12.4	941	6	US-10-501-035-343
20	277.5	11.5	854	6	US-10-511-657-4
21	191	7.9	786	7	US-11-072-512-2944
22	103	4.3	968	6	US-10-501-035-219
23	94.5	3.9	611	7	US-11-087-099-8358
24	91.5	3.8	635	7	US-11-096-568A-29628
25	91.5	3.8	710	7	US-11-096-568A-29627

26	90	3.7	1049	7	US-11-137-465-42	Sequence 42, Appli
27	86	3.6	418	7	US-11-109-156-2	Sequence 2, Appli
28	83.5	3.5	937	7	US-11-096-568A-31319	Sequence 31319, A
29	82.5	3.4	422	7	US-11-230-251-26	Sequence 26, Appli
30	82	3.4	366	7	US-11-096-568A-5564	Sequence 5564, Ap
31	82	3.4	372	7	US-11-096-568A-5563	Sequence 5563, Ap
32	82	3.4	643	7	US-11-096-568A-27797	Sequence 27797, A
33	82	3.4	1024	6	US-10-131-826A-198	Sequence 198, App
34	82	3.4	1024	6	US-10-973-115B-198	Sequence 198, App
35	81.5	3.4	808	7	US-11-072-512-2324	Sequence 2324, Ap
36	81	3.4	286	7	US-11-072-512-2361	Sequence 3361, Ap
37	81	3.4	418	7	US-11-099-691-1	Sequence 1, Appli
38	81	3.4	484	7	US-11-072-512-3381	Sequence 3381, Ap
39	81	3.4	678	7	US-11-072-512-3832	Sequence 3832, Ap
40	81	3.4	852	6	US-10-467-657-5004	Sequence 5004, Ap
41	81	3.4	926	7	US-11-232-405A-34	Sequence 34, Appli
42	81	3.4	6738	6	US-10-922-232B-56	Sequence 56, Appli
43	80.5	3.3	326	7	US-11-087-099-1590	Sequence 1590, Ap
44	80.5	3.3	376	7	US-11-098-686-10379	Sequence 10379, A
45	80.5	3.3	3487	7	US-11-087-099-10423	Sequence 10423, A

## ALIGNMENTS

RESULT 1  
US-11-226-701-4  
; Sequence 4, Application US/11226701  
; Publication No. US2006009632A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: NOVEL 27875, 22035, 27420, 17906, 16319,  
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: WPI03-0210NMIM  
; CURRENT APPLICATION NUMBER: US/11/226,701  
; PRIOR FILING DATE: 2005-09-14  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 2000-05-16  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2000-05-16  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR FILING DATE: 2001-12-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-226-701-4

Query Match 93.8%; Score 2258; DB 7; Length 502;  
Best Local Similarity 100.0%; Pred. No. 9.2e-201; Indels 0; Gaps 0;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDTRLRGQTGVRAERRGSYPFIDFRLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87  
Db 80 GDTRLRGQTGVRAERRGSYPFIDFRLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 207  
Db 200 FKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 259

Qy 208 LAAAAHDVDPGVNQPFLLIKTNHHLANLYQNMVLENHNRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVDPGVNQPFLLIKTNHHLANLYQNMVLENHNRSTIGMLRESRLLAHLPKEM 319

Qy 268 TDIEEQGLSLIATDINRQNEFLTRUKAHLHNKDLFEADAQRHFMQLTALKCADICNP 327  
Db 320 TDIEEQGLSLIATDINRQNEFLTRUKAHLHNKDLFEADAQRHFMQLTALKCADICNP 379

Qy 328 CRIWEMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVPELPR 387  
Db 380 CRIWEMSKQWSEVCEFYRQGELEQKFELEISPLCNQKDSIPSIQIGFMSYIVPELPR 439

Qy 388 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQHRSGSGSGSPGDHDHAGQGTSEBEQEG 447  
Db 440 EWAHFTGNSTLSENMLGHLAHNAQWKSLLPRQHRSGSGSGSPGDHDHAGQGTSEBEQEG 499

Qy 448 DSP 450  
Db 500 DSP 502

RESULT 2

US-11-226-701-6  
; Sequence 6, Application US/11226701  
; Publication No. US2006009632A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Mlyoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MPI03-0210WNIM  
; CURRENT APPLICATION NUMBER: US/11/226,701  
; CURRENT FILING DATE: 2005-09-14  
; PRIOR APPLICATION NUMBER: US/10/386,414  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: 09/426,282  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 09/668,266  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/330,970  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: 09/724,599  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/860,193  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/571,689  
; PRIOR FILING DATE: 2000-05-16  
; PRIOR APPLICATION NUMBER: 10/283,023

Query Match 53.2%; Score 1280; DB 7; Length 320;  
Best Local Similarity 100.0%; Pred. No. 1.3e-110; Indels 0; Gaps 0;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDTRLRGQTGVRAERRGSYPFIDFRLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLRG 87  
Db 80 GDTRLRGQTGVRAERRGSYPFIDFRLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLRG 139

Qy 88 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 147  
Db 140 IIPQAPLHLLDEYLGQARHMLSKVGWMDFDIFLFDRLTNGNSLVTLCHLFNTHGLIHH 199

Qy 148 FKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 207  
Db 200 FKLDVMTLHRLFLVMQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGL 259

Qy 208 LAAAAHDVDPGVNQPFLLIKTNHHLANLYQNMVLENHNRSTIGMLRESRLLAHLPKEM 267  
Db 260 LAAAAHDVDPGVNQPFLLIKTNHHLANLYQNMVLENHNRSTIGMLRESRLLAHLPKEM 319

Qy 268 T 268  
Db 320 T 320

RESULT 3

US-11-091-018-10  
; Sequence 10, Application US/11091018  
; Publication No. US20050287551A1  
; GENERAL INFORMATION:  
; APPLICANT: Gretaardottir, Solveig  
; APPLICANT: Thorleifsson, Gudmar  
; APPLICANT: Gulcher, Jeffrey R.  
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;  
; FILE REFERENCE: 2345.2010-016  
; CURRENT APPLICATION NUMBER: US/11/091,018  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: PCT/US03/29906  
; PRIOR FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 10/255,120  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: 10/419,723  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 10/650,120  
; PRIOR FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: 10/067,514  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 09/811,352  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-091-018-10

Query Match 25.1%; Score 604.5; DB 7; Length 507;

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Best Local Similarity 33.3%; Pred. No. 6.8e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 52 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTEQEDVLAKB---LEDVNKWLHVFR 108
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDVHSQNPYHNAVHAAD 180
Db 109 IABL-SGNRPLTVIMHTIPOERDLLTKFKIPVDLTILYMLTEHDYHADVAYHNNIHAAD 167
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
Db 168 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVNQPFLINTNSSELALMYNDSS 227
Qy 241 VLENHWRSTIGMLRESR--LLAHLPEKMTQDIEQQGLSLILATDINRQNEFLTRLKAHL 298
Db 228 VLENHHLAVGFKLQEBENCDFQNLTKQQRSLRKWVIDIVLATDMSKHNLLADLKTVM 287
Qy 299 HNKD-----LRLEDAQRHFMLOIALKCADICNPGRIMWMSKOWSERVCEEFYRQGELE 352
Db 288 ETKKVTSSGVLDDNYSRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIIMEEFPQGDRE 347
Qy 353 QKFELEISPLCNOQKQDIPSIGIFMSYIIEPLFREWHAFTGNSTSENMLGLHNAKQA 412
Db 348 RERGMEISPMCDKHNAVESKSVQGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 405
Qy 413 WKSLPQRHRSRSGSGGPDHAGQGTSE-----EQEGDS 449
Db 406 YQSTIPQ-----SPSPAPDDPEGRQGTKEQFELTLEEDGES 444

RESULT 4
US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091.018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-08-27
; PRIOR FILING DATE: 2002-02-04
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-08-27
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-9

Query Match 25.1%; Score 604.5; DB 7; Length 585;
Best Local Similarity 33.3%; Pred. No. 8.2e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 130 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTEQEDVLAKB---LEDVNKWLHVFR 186

Best Local Similarity 33.3%; Pred. No. 6.8e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 218 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTEQEDVLAKB---LEDVNKWLHVFR 274
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDVHSQNPYHNAVHAAD 180
Db 275 IABL-SGNRPLTVIMHTIPOERDLLTKFKIPVDLTILYMLTEHDYHADVAYHNNIHAAD 333
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
Db 334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVNQPFLINTNSSELALMYNDSS 393

Best Local Similarity 33.3%; Pred. No. 9.9e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVRLLS----FQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFL 121
Db 218 KKKKRPMSQISGVKLMHSSSLTNSSIPRFGVKTEQEDVLAKB---LEDVNKWLHVFR 274
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDVHSQNPYHNAVHAAD 180
Db 275 IABL-SGNRPLTVIMHTIPOERDLLTKFKIPVDLTILYMLTEHDYHADVAYHNNIHAAD 333
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
Db 334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVNQPFLINTNSSELALMYNDSS 393
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Db 354 KKKKRPMSQISGVKKLHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVP 410  
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMQEDVHSQNPYHNAHAAD 180  
Db 411 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTMLTLEDHYHADVAYHNNHAAD 469  
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHDPGVNQPFLIKTNHHLANLYONMS 240  
Db 470 VVQSTHVLLSTPALEAVFTDLAIAFASAIHDVDPGVSNQFLINTNSELAMYNDS 529  
Qy 241 VLENHHRSTIGMLRESR--LLAHLPKEMTDIEQOLGSLILATDINRQNEFTRLKAHL 298  
Db 530 VLENHHLAVGFKLQEBNCDFQNLTKKQSLRKWVIDVLATDMSKMNLLADLKTWV 589  
Qy 299 HNKD-----LRLEDAQDRHFMQLKADICNPCRIMWSKQWSEVCEEFYRQGELE 352  
Db 590 ETQKVTSSGVLLLDNYSRDIQVLQNMVHCADLSNPTKPLQLYRQWTDRIWEEFFRQGDRE 649  
Qy 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIPEPLFREWAHFTGNSTSENMLGLAHNAKQ 412  
Db 650 RERGMESPMCKHNASVEKSGVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 707  
Qy 413 WKSLLPRQHRSGSGSPDHDHAGQGTSE-----EQEGDS 449  
Db 708 YQSTIPQ-----SPSPAPDDPEGQGTQKQFQFELTLEEDGES 746

## RESULT 11

US-10-492-835-8  
; Sequence 8, Application US/10492835  
; Publication No. US20050289660A2  
; GENERAL INFORMATION:  
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION  
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS  
; FILE REFERENCE: MEMORY 4 WO  
; CURRENT APPLICATION NUMBER: US/10/492, 835  
; CURRENT FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; LENGTH: 747  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-492-835-8

Query Match 25.1%; Score 603.5; DB 6; Length 747;  
Best Local Similarity 33.3%; Pred. No. 1.4e-47;  
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;  
Qy 66 KKKVKLLS-----FQRYFHASRLRGIIPQAPLHLDDEDYLGQARHMLSKVGMWDFDIFL 121  
Db 293 KKKKRPMSQISGVKKLHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVP 349  
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMQEDVHSQNPYHNAHAAD 180  
Db 350 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTMLTLEDHYHADVAYHNNHAAD 408  
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHDPGVNQPFLIKTNHHLANLYONMS 240  
Db 409 VVQSTHVLLSTPALEAVFTDLAIAFASAIHDVDPGVSNQFLINTNSELAMYNDS 468  
Qy 241 VLENHHRSTIGMLRESR--LLAHLPKEMTDIEQOLGSLILATDINRQNEFTRLKAHL 298  
Db 469 VLENHHLAVGFKLQEBNCDFQNLTKKQSLRKWVIDVLATDMSKMNLLADLKTWV 528  
Qy 299 HNKD-----LRLEDAQDRHFMQLKADICNPCRIMWSKQWSEVCEEFYRQGELE 352  
Db 529 ETQKVTSSGVLLLDNYSRDIQVLQNMVHCADLSNPTKPLQLYRQWTDRIWEEFFRQGDRE 588  
Qy 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIPEPLFREWAHFTGNSTSENMLGLAHNAKQ 412

Db 589 RERGMESPMCKHNASVEKSGVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646  
Qy 413 WKSLLPRQHRSGSGSPDHDHAGQGTSE-----EQEGDS 449  
Db 647 YQSTIPQ-----SPSPAPDDPEGQGTQKQFQFELTLEEDGES 685  
RESULT 12  
US-10-492-835-27  
; Sequence 27, Application US/10492835  
; Publication No. US20050289660A2  
; GENERAL INFORMATION:  
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION  
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS  
; FILE REFERENCE: MEMORY 4 WO  
; CURRENT APPLICATION NUMBER: US/10/492, 835  
; CURRENT FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 27  
; LENGTH: 747  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-492-835-27

Query Match 25.1%; Score 603.5; DB 6; Length 747;  
Best Local Similarity 33.3%; Pred. No. 1.4e-47;  
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;  
Qy 66 KKKVKLLS-----FQRYFHASRLRGIIPQAPLHLDDEDYLGQARHMLSKVGMWDFDIFL 121  
Db 293 KKKKRPMSQISGVKKLHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVKNKGLHVP 349  
Qy 122 FDLRTNGNSLVTLCH-LFNTHGLIHFKLDMVTLHRFLVMQEDVHSQNPYHNAHAAD 180  
Db 350 IAEI-SGNRPLTVIMHTIFQERDLTKFKIPVDLTLYLTMLTLEDHYHADVAYHNNHAAD 408  
Qy 181 VTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHDPGVNQPFLIKTNHHLANLYONMS 240  
Db 409 VVQSTHVLLSTPALEAVFTDLAIAFASAIHDVDPGVSNQFLINTNSELAMYNDS 468  
Qy 241 VLENHHRSTIGMLRESR--LLAHLPKEMTDIEQOLGSLILATDINRQNEFTRLKAHL 298  
Db 469 VLENHHLAVGFKLQEBNCDFQNLTKKQSLRKWVIDVLATDMSKMNLLADLKTWV 528  
Qy 299 HNKD-----LRLEDAQDRHFMQLKADICNPCRIMWSKQWSEVCEEFYRQGELE 352  
Db 529 ETQKVTSSGVLLLDNYSRDIQVLQNMVHCADLSNPTKPLQLYRQWTDRIWEEFFRQGDRE 588  
Qy 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIPEPLFREWAHFTGNSTSENMLGLAHNAKQ 412  
Db 589 RERGMESPMCKHNASVEKSGVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646  
Qy 413 WKSLLPRQHRSGSGSPDHDHAGQGTSE-----EQEGDS 449  
Db 647 YQSTIPQ-----SPSPAPDDPEGQGTQKQFQFELTLEEDGES 685

## RESULT 13

US-10-492-835-15  
; Sequence 15, Application US/10492835  
; Publication No. US20050289660A2  
; GENERAL INFORMATION:  
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION  
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS  
; FILE REFERENCE: MEMORY 4 WO  
; CURRENT APPLICATION NUMBER: US/10/492, 835  
; CURRENT FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 15

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; LENGTH: 747
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-492-835-15

Query Match      24.7%; Score 594.5; DB 6; Length 747;
Best Local Similarity 33.4%; Pred. No. 9.6e-47;
Matches 131; Conservative 84; Mismatches 152; Indels 25; Gaps 8;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPQAPLHLLDEYDYGQARHMLSKVGMWDFDIFL 121
Db 293 KKKVKRMSQISGVKKLHSSSLTNSCIPRFQVTEQEDVLAXE---LEDVKNKGLHVR 349
Qy 122 FDLRTNGSLVTLTLLCH-LFNTHGLIHFHKLDMVTLHRLVVMVQEDYHSQNPYHNAVHAAD 180
Db 350 TAEI-SGNRPITVIMHTIFQERDLTKIPVDITLITVMTLEDDHYADVAHYNNIHAAD 408
Qy 181 VTQAMHCYLKEPKLASFLTPDIDMLGLLAAAHDVDPGVNQPFLLKTNHHLANLYQWMS 240
Db 409 VQSTHVLSTPALEAVFTDLEILAAIFASAIHVDVDPGVNQFLINTNSALALMYNDSS 468
Qy 241 VLENHWRSTIGMLRESR--LLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRLKAHL 298
Db 469 VLENHHLAVGFKLQEECDIFQNLTKKQRLKQWIDIVLATDMSKHNLLADLTKTW 528
Qy 299 HNKD-----LRLEDAQRHFMQLKACDINCPRIWEMSKQWSEVCEEFYRQGELE 352
Db 529 ETKKVTSSGVLLDNYSDRIQVLMVHCADLSNPTKPLQIYRWQTDRIWEEFPRQGDRE 588
Qy 353 QKPELISPLCNOQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGLHNAKQAQ 412
Db 589 RERGMEISPMCDKNNAFVEKSVQGFIDYIVHPLWETWADLV--HPQAQDILDTLEDNREW 646
Qy 413 WKSLLPRQHRSGSGSGGPDHDHAGQGTSESE 444
Db 647 YQSTIPIQ-----SPSPAPDDPEGRQGTQTEK 672

RESULT 14
US-11-123-893-13
; Sequence 13, Application US/11123893
; Publication No. US20060041006A1
; GENERAL INFORMATION:
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: CHO, HANNA
; APPLICANT: ENGLAND, BRUCE
; APPLICANT: GILLETTE, SAM
; APPLICANT: ARTIS, DEAN RICHARD
; APPLICANT: ZUCKERMAN, REBECCA
; APPLICANT: ZHANG, CHAO
; TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
; FILE REFERENCE: 039363-1109
; CURRENT APPLICATION NUMBER: US/11/123.893
; CURRENT FILING DATE: 2005-05-06
; PRIOR FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 13
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-123-893-13

Query Match      23.7%; Score 570.5; DB 7; Length 349;
Best Local Similarity 34.4%; Pred. No. 5.6e-45;
Matches 122; Conservative 77; Mismatches 135; Indels 21; Gaps 7;

Qy 99 EDYLGQARHMLSKVGMWDFDIFLFDRLTNGSLVTLTLLCH-LFNTHGLIHFHKLDMVTLHR 157
Db 4 EDVLAK-----LEDVKNKGLHVFRIAEI-SGNRPITVIMHTIFQERDLTKFKIPVDTLIT 59
Qy 158 FLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPDIDMLGLLAAAHDVVDH 217

; LENGTH: 747
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-492-835-15

Query Match      24.7%; Score 594.5; DB 6; Length 747;
Best Local Similarity 33.4%; Pred. No. 9.6e-47;
Matches 131; Conservative 84; Mismatches 152; Indels 25; Gaps 8;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPQAPLHLLDEYDYGQARHMLSKVGMWDFDIFL 121
Db 293 KKKVKRMSQISGVKKLHSSSLTNSCIPRFQVTEQEDVLAXE---LEDVKNKGLHVR 349
Qy 122 FDLRTNGSLVTLTLLCH-LFNTHGLIHFHKLDMVTLHRLVVMVQEDYHSQNPYHNAVHAAD 180
Db 350 TAEI-SGNRPITVIMHTIFQERDLTKIPVDITLITVMTLEDDHYADVAHYNNIHAAD 408
Qy 181 VTQAMHCYLKEPKLASFLTPDIDMLGLLAAAHDVDPGVNQPFLLKTNHHLANLYQWMS 240
Db 409 VQSTHVLSTPALEAVFTDLEILAAIFASAIHVDVDPGVNQFLINTNSALALMYNDSS 468
Qy 241 VLENHWRSTIGMLRESR--LLAHLPKEMTQDIEQOLGSLILATDINRQNEFLTRLKAHL 298
Db 469 VLENHHLAVGFKLQEECDIFQNLTKKQRLKQWIDIVLATDMSKHNLLADLTKTW 528
Qy 299 HNKD-----LRLEDAQRHFMQLKACDINCPRIWEMSKQWSEVCEEFYRQGELE 352
Db 529 ETKKVTSSGVLLDNYSDRIQVLMVHCADLSNPTKPLQIYRWQTDRIWEEFPRQGDRE 588
Qy 353 QKPELISPLCNOQKDSIPSIQIGFMSYIVPELFRWAHFTGNSTLSENMLGLHNAKQAQ 412
Db 589 RERGMEISPMCDKNNAFVEKSVQGFIDYIVHPLWETWADLV--HPQAQDILDTLEDNREW 646
Qy 413 WKSLLPRQHRSGSGSGGPDHDHAGQGTSESE 444
Db 647 YQSTIPIQ-----SPSPAPDDPEGRQGTQTEK 672

RESULT 15
US-11-169-041-207
; Sequence 207, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169.041
; CURRENT FILING DATE: 2005-06-28
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
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; SEQ ID NO 207
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-207

Query Match      23.6%; Score 567.5; DB 7; Length 736;
Best Local Similarity 31.3%; Pred. No. 3e-44;
Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

Qy 66 KKKVKRLLS-----FQRYFHASRLRLGIIPQAPLHLLDEYDYGQARHMLSKVGMWDFDIFL 121
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Job time : 18.6829 secs